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OM protein - protein search, using sw model

Run on: August 26, 2003, 15:40:52 ; Search time 88 Seconds
(without alignments)
1242.757 Million cell updates/sec

Title: US-10-052-664-1

Perfect score: 3597

Sequence: 1 MAPWPELGDAQPNPKYLEG.....SREAGYVPSDSKTECTAL 689

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 13Jun03;*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
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- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	3597	100.0	689	21	AA18613
2	3594	99.9	689	22	ABB50299
3	3589	99.8	689	23	ABG96383
4	3581.5	99.6	690	22	AAW78631
5	3581.5	99.6	700	22	ABB12311
6	3581.5	99.6	700	22	AAW79615
7	3570.5	99.3	690	19	AAW77414
8	3240	90.1	631	22	AAW93865
9	2098	58.3	397	22	AAW93860

10	1529	42.5	599	22	AAE06591	Human protein havi
11	742	20.6	155	19	AAW77415	Human sodium depen
12	418.5	11.6	388	23	AAQ92763	C Glutamicum prote
13	410	11.4	411	22	AAW76765	Corynebacterium gl
14	280.5	7.8	549	23	ABP29511	Streptococcus poly
15	274.5	7.6	544	23	ABB47553	Listeria monocytog
16	263.5	7.3	543	24	ABU08131	Streptococcus pneu
17	263.5	7.3	543	24	ABU08059	S. pneumoniae type
18	183.5	5.1	120	19	AAW77597	Possible sodium-de
19	142.5	4.0	441	23	ABB47592	Listeria monocytog
20	133.5	3.7	443	23	ABB48414	Listeria monocytog
21	131.5	3.7	90	22	ABG27784	Novel human diagno
22	130.5	3.6	74	22	ABG23596	Novel human diagno
23	130.5	3.6	74	22	ABG23597	Novel human diagno
24	130.5	3.6	74	22	ABG23601	Novel human diagno
25	129.5	3.6	886	23	AAE16785	Human transporter
26	128.5	3.6	524	22	AAU54281	Propionibacterium
27	128.5	3.6	556	24	ABB82976	Human SLC22A relat
28	128.5	3.6	565	22	ABG11289	Novel human diagno
29	128.5	3.6	565	22	ABG11291	Novel human diagno
30	127.5	3.5	701	23	AAE24209	Rat obesity-specif
31	126.5	3.5	307	24	ABP81373	Streptococcus pneu
32	126.5	3.5	307	24	ABU01250	S. pneumoniae type
33	126.5	3.5	517	23	ABF66239	Bifidobacterium lo
34	126	3.5	398	22	ABG19008	Novel human diagno
35	125.5	3.5	1743	24	ABU07906	Novel human secret
36	125	3.5	547	23	ABG93114	S. cerevisiae BAX-
37	124.5	3.5	456	24	ABJ19067	Pathogen specific
38	122	3.4	122	22	ABG27074	Novel human diagno
39	122	3.4	130	22	ABG23598	Novel human diagno
40	122	3.4	130	22	ABG27785	Human transporter
41	121.5	3.4	509	23	ABG83901	Human transporter
42	121.5	3.4	509	23	ABG61543	Drosophila melanog
43	121.5	3.4	896	22	ABG63778	Novel human diagno
44	121	3.4	89	22	ABG27446	Streptococcus poly
45	120	3.3	728	23	ABP26246	

ALIGNMENTS

RESULT 1
AA18613
ID AA18613 standard; Protein, 689 AA.
XX
AC AA18613;
XX
DT 15-JAN-2001 (first entry)
XX
DE A human sodium phosphate cotransporter, designated Npt2B.
XX
KW Human; sodium phosphate cotransporter; Npt2B; intestinal epithelial cell;
KW phosphate absorption; inorganic phosphate metabolism; phosphatemia;
KW osteomalacia; rickets; hyperparathyroidism; renal disease.
XX
OS Homo sapiens.
XX
PN AU200014979-A.
XX
PD 31-AUG-2000.
XX
PF 09-FEB-2000; 2000AU-0014979.
XX
PR 09-FEB-1999; 99US-0119321.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Cannon PD, Sankurati S;
XX
DR WPI; 2000-579513/55.
XX
DR N-PSDB; AAA75484.
XX
PT Human sodium-phosphate cotransporter Npt2B, useful e.g. for identifying

Best Local Similarity 99.9%; Pred. No. 0;		Matches 688; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MAWPBLGDAQNPDKYLEGAGQQTAPDKSKETNKNTAPVTKIELLPSTATLID	60
Db	1	MAWPBLGDAQNPDKYLEGAGQQTAPDKSKETNKNTAPVTKIELLPSTATLID	60
QY	61	EPTVEDDPNNLPTLQDSGKWSERDTGKILCFQGIKRLILGFLYFFVCSLDILSSA	120
Db	61	EPTVEDDPNNLPTLQDSGKWSERDTGKILCFQGIKRLILGFLYFFVCSLDILSSA	120
QY	121	FQLVGKMGAGOFFNSNSIMSNPLGLVIGLVTLVQSSSTSTSVVSMVSSLLVRAA	180
Db	121	FQLVGKMGAGOFFNSNSIMSNPLGLVIGLVTLVQSSSTSTSVVSMVSSLLVRAA	180
QY	181	IPILMGANTGTSITNTIIVALMOVDRSEFRAPAGATVHDFNWLVLVPLVEVATHYL	240
Db	181	IPILMGANTGTSITNTIIVALMOVDRSEFRAPAGATVHDFNWLVLVPLVEVATHYL	240
QY	241	EIITQILVSEFFKNGEDAPDLKXVITKPTKLIIVQLODKVLSOLAMNDEKAKNSLVKI	300
Db	241	EIITQILVSEFFKNGEDAPDLKXVITKPTKLIIVQLODKVLSOLAMNDEKAKNSLVKI	300
QY	301	WCKTFNKTQINVTVPSTANTCPSLCWTDGIONTMKNVYKXENIAKCOHIFVNFHLPD	360
Db	301	WCKTFNKTQINVTVPSTANTCPSLCWTDGIONTMKNVYKXENIAKCOHIFVNFHLPD	360
QY	361	LAVGTILLILSLVLCGLIMVILKGLSVLKGQVATVTKTINTDPFPFANLTGYLAL	420
Db	361	LAVGTILLILSLVLCGLIMVILKGLSVLKGQVATVTKTINTDPFPFANLTGYLAL	420
QY	421	VGAGMTFIVQSSSVFTSALTPLIGVITITERAYPLTIGSNITGTTTALLAALASFGNAL	480
Db	421	VGAGMTFIVQSSSVFTSALTPLIGVITITERAYPLTIGSNITGTTTALLAALASFGNAL	480
QY	481	RSSIQIALCHFFPFIISGILLWYPPFRLPIRMAKGLGNISAKYRWFAVFIILIFFFLIP	540
Db	481	RSSIQIALCHFFPFIISGILLWYPPFRLPIRMAKGLGNISAKYRWFAVFIILIFFFLIP	540
QY	541	LTVFGLSLAGVAVGVGVVVFVFIILVLCRLQSCRPVLPKLQNNWFLPLWRSILK	600
Db	541	LTVFGLSLAGVAVGVGVVVFVFIILVLCRLQSCRPVLPKLQNNWFLPLWRSILK	600
QY	601	PWDAVSKTGFQFQRCOCRCVCCACCLLCCPKCCRCCKCCEDEEAKQGDVPVKA	660
Db	601	PWDAVSKTGFQFQRCOCRCVCCACCLLCCPKCCRCCKCCEDEEAKQGDVPVKA	660
QY	661	PETFDNITISREAQGEVPASDSKTECTAL	689
Db	661	PETFDNITISREAQGEVPASDSKTECTAL	689
RESULT 3			
ABG96383			
ID	ABG96383 standard; Protein; 689 AA.		
XX	AC ABG96383;		
XX	DT 11-DEC-2002 (first entry)		
XX	DE Human ovarian cancer marker M463.		
KW	Human; ovarian cancer; marker; cancer; familial history; brain disorder;		
KW	Central nervous system disorder; bacterial meningitis; viral meningitis;		
KW	Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;		
KW	brain herniation; inflammation; encephalitis; testicular disorder;		
KW	nontuberculous granulomatous orchitis; connective tissue disorder;		
KW	heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;		
KW	histological type; carcinogenic; ovarian cancer marker.		
OS	Homo sapiens.		
XX	WO200271928-A2.		
PN			

XX	19-SEP-2002.	
PD		
XX	14-MAR-2002; 2002WO-US07826.	
XX	14-MAR-2001; 2001US-276025P.	
PR	14-MAR-2001; 2001US-276026P.	
PR	10-AUG-2001; 2001US-311732P.	
PR	19-SEP-2001; 2001US-323580P.	
PR	26-SEP-2001; 2001US-324967P.	
PR	26-SEP-2001; 2001US-325102P.	
PR	26-SEP-2001; 2001US-325149P.	
XX	(MILL-) MILLENNIUM PHARM INC.	
XX	Monahan JE, Ganavarrapu M, Hoersch S, Kamatkar S, Kovatis SG;	
PI	Meyers RE, Morrissey MP, Olandt PU, Sen A, Vieby PO, Mills GB;	
PI	Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;	
XX	WPI; 2002-723277/78.	
DR	N-PSDB; ABS76479.	
XX	Assessing whether a patient is afflicted with ovarian cancer, useful in	
PT	assessing the stage or progression of the disease, comprises comparing	
PT	the expression level of a cancer marker in a sample from a patient and	
PT	from a non cancer patient -	
XX	Disclosure; Page 349-351; 481pp; English.	
PS	The present invention relates to a new method for assessing whether a	
XX	patient is afflicted with ovarian cancer. The method involves comparing	
CC	the expression level of a marker in a patient sample and the normal level	
CC	of expression of the marker in a control non-ovarian cancer sample, where	
CC	the marker is selected from 363 cancer markers described in the	
CC	specification. The method of the invention is useful in diagnosing or	
CC	characterising cancer, in detecting the presence of cancer as early as	
CC	possible, and the recurrence of ovarian cancer. The method may also be of	
CC	particular use with patients having an enhanced risk of developing	
CC	ovarian cancer (e.g. patients having a familial history of ovarian	
CC	cancer). The cancer markers may be used in the management and treatment	
CC	of e.g. brain and central nervous system disorders (e.g. bacterial and	
CC	viral meningitis, Alzheimer's disease or Parkinson's disease), brain	
CC	inflammations (e.g. cerebral oedema, hydrocephalus or brain herniations),	
CC	testicular disorders (e.g. bacterial or viral meningitis or encephalitis),	
CC	connective tissue disorders, or heart disorders (e.g. ischaemic heart	
CC	disease or atherosclerosis). The compositions and methods may also be	
CC	used in assessing the histological type of neoplasm associated with	
CC	ovarian cancer, monitoring the progression of ovarian cancer,	
CC	determining whether ovarian cancer has metastasized or is likely to	
CC	metastasize, selecting a composition for inhibiting ovarian cancer,	
CC	assessing the ovarian carcinogenic potential of a compound, or	
CC	inhibiting ovarian cancer or at risk of developing ovarian cancer. The	
CC	present amino acid sequence represents one of the ovarian cancer markers	
CC	described in the invention.	
XX	Sequence 689 AA;	
SQ	Query Match 99.8%; Score 3589; DB 23; Length 689;	
	Best Local Similarity 99.7%; Pred. No. 0;	
	Matches 687; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	1	MAWPBLGDAQNPDKYLEGAGQQTAPDKSKETNKNTAPVTKIELLPSTATLID 60
Db	1	MAWPBLGDAQNPDKYLEGAGQQTAPDKSKETNKNTAPVTKIELLPSTATLID 60
QY	61	EPTVEDDPNNLPTLQDSGKWSERDTGKILCFQGIKRLILGFLYFFVCSLDILSSA 120
Db	61	EPTVEDDPNNLPTLQDSGKWSERDTGKILCFQGIKRLILGFLYFFVCSLDILSSA 120
QY	121	FQLVGKMGAGOFFNSNSIMSNPLGLVIGLVTLVQSSSTSTSVVSMVSSLLVRAA 180
Db	121	FQLVGKMGAGOFFNSNSIMSNPLGLVIGLVTLVQSSSTSTSVVSMVSSLLVRAA 180

QY 181 IPIINGANIGTSITNTIIVLMQVGRSEFRAPAGATVHDFNNLSVLVLLPVEVATHYL 240
 Db 181 IPIINGANIGTSITNTIIVLMQVGRSEFRAPAGATVHDFNNLSVLVLLPVEVATHYL 240
 QY 241 EIITQIIVSFHFHFKNGEDAPDLKVTIKPFTKLIVQLDKKVISQIAMNDEKAKNKSIVKI 300
 Db 241 EIITQIIVSFHFHFKNGEDAPDLKVTIKPFTKLIVQLDKKVISQIAMNDEKAKNKSIVKI 300
 QY 301 WCKTFTNKTOINVTVPSTANCTSPSLCWTGDIQNWTKMKNVTYKENTIAKCOHIFVNFHLPD 360
 Db 301 WCKTFTNKTOINVTVPSTANCTSPSLCWTGDIQNWTKMKNVTYKENTIAKCOHIFVNFHLPD 360
 QY 361 LAVGTILLILSLVLGCLIMIVKILGSLVKGQVATVTKTINTDPPPPFAWLGYLAIL 420
 Db 361 LAVGTILLILSLVLGCLIMIVKILGSLVKGQVATVTKTINTDPPPPFAWLGYLAIL 420
 QY 421 VQAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTIGSNIGTTTTTALALASPQNAL 480
 Db 421 VQAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTIGSNIGTTTTTALALASPQNAL 480
 QY 481 RSSIQIALCHFFFNISGILLWYPIPTPLIRMAKGLGNISAKYRFAVYLIIFFFLIP 540
 Db 481 RSSIQIALCHFFFNISGILLWYPIPTPLIRMAKGLGNISAKYRFAVYLIIFFFLIP 540
 QY 541 LTVFGLSLAGRWLVGVGVVVFIIILVLCRLQLQSCRPVLPKQLQNNWFLPLMWSLK 600
 Db 541 LTVFGLSLAGRWLVGVGVVVFIIILVLCRLQLQSCRPVLPKQLQNNWFLPLMWSLK 600
 QY 601 PWDVSKFTGCFQMRCCCCVCCVCCACLLCGCPKCCRCCKEDLEAQRGQDVPVKA 660
 Db 601 PWDVSKFTGCFQMRCCCCVCCVCCACLLCGCPKCCRCCKEDLEAQRGQDVPVKA 660
 QY 661 PETFDNITISREAGVFPASDSKTECTAL 689
 Db 661 PETFDNITISREAGVFPASDSKTECTAL 689
 RESULT 4
 AAM78631
 ID AAM78631 standard; Protein; 690 AA.
 XX AC AAM78631;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human protein SEQ ID NO 1293.
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX OS Homo sapiens.
 XX PN WO200157190-A2.
 XX PD 09-AUG-2001.
 XX PF 05-FEB-2001; 2001WO-US04098.
 XX PR 03-FEB-2000; 2000US-0496914.
 XX PR 27-APR-2000; 2000US-05060875.
 XX PR 20-JUN-2000; 2000US-0598075.
 XX PR 19-JUL-2000; 2000US-0620325.
 XX PR 01-SEP-2000; 2000US-0654936.
 XX PR 13-SEP-2000; 2000US-0663361.
 XX PR 20-OCT-2000; 2000US-0693325.
 XX PR 30-NOV-2000; 2000US-0728422.
 XX PA (HYSE-) HYSEQ INC.
 XX PT Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;

PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZH;
 PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
 XX DR WPI; 2001-476283/51.
 XX DR N-PSDB; AAK51764.
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 useful in diagnosis and gene therapy -
 XX Claim 20; Page 3546-3548; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX SQ Sequence 690 AA;
 Query Match 99.6%; Score 3581.5; DB 22; Length 690;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 688; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MAPPELGDQAPNDPKYLEGAGGOPTAPDKSKETNK-NNTEAPVTIKELLPVSTATLI 59
 Db 1 MAPPELGDQAPNDPKYLEGAGGOPTAPDKSKETNKNDTEAPVTIKELLPVSTATLI 60
 QY 60 DEPTVEDDPNLTQDSGIKWSERDTKGILCFQGIKRLILLGLFLYFVCSLDILSS 119
 Db 61 DEPTVEDDPNLTQDSGIKWSERDTKGILCFQGIKRLILLGLFLYFVCSLDILSS 120
 QY 120 AFQLVGNKAGOFFNSNSINPNLLGLIVGLVTVLVVQSSSTSTSIIVSMVSSSLTVRA 179
 Db 121 AFQLVGNKAGOFFNSNSINPNLLGLIVGLVTVLVVQSSSTSTSIIVSMVSSSLTVRA 180
 QY 180 AIPILMGANIGTSITNTIIVLMQVGRSEFRAPAGATVHDFNNLSVLVLLPVEVATHY 239
 Db 181 AIPILMGANIGTSITNTIIVLMQVGRSEFRAPAGATVHDFNNLSVLVLLPVEVATHY 240
 QY 240 LEIITQIIVSFHFHFKNGEDAPDLKVTIKPFTKLIVQLDKKVISQIAMNDEKAKNKSIVK 299
 Db 241 LEIITQIIVSFHFHFKNGEDAPDLKVTIKPFTKLIVQLDKKVISQIAMNDEKAKNKSIVK 300
 QY 300 IWCKTFTNKTOINVTVPSTANCTSPSLCWTGDIQNWTKMKNVTYKENTIAKCOHIFVNFHLP 359
 Db 301 IWCKTFTNKTOINVTVPSTANCTSPSLCWTGDIQNWTKMKNVTYKENTIAKCOHIFVNFHLP 360
 QY 360 DLAVGTILLILSLVLGCLIMIVKILGSLVKGQVATVTKTINTDPPPPFAWLGYLAI 419
 Db 361 DLAVGTILLILSLVLGCLIMIVKILGSLVKGQVATVTKTINTDPPPPFAWLGYLAI 420
 QY 420 LVGAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTIGSNIGTTTTTALALASPQNA 479
 Db 421 LVGAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTIGSNIGTTTTTALALASPQNA 480
 QY 480 LRSLQIALCHFFFNISGILLWYPIPTPLIRMAKGLGNISAKYRFAVYLIIFFFLIP 539
 Db 481 LRSLQIALCHFFFNISGILLWYPIPTPLIRMAKGLGNISAKYRFAVYLIIFFFLIP 540
 QY 540 PLTVFGLSLAGRWLVGVGVVVFIIILVLCRLQLQSCRPVLPKQLQNNWFLPLMWSLK 599
 Db 541 PLTVFGLSLAGRWLVGVGVVVFIIILVLCRLQLQSCRPVLPKQLQNNWFLPLMWSLK 600
 QY 600 KPMADVSKFTGCFQMRCCCCVCCVCCACLLCGCPKCCRCCKEDLEAQRGQDVPVKA 659

Db 601 KPDAVSKFTGCEQWCCCRVCCACCLCGCPKCCCKCELEAEQAGQDVPYK 660
 QY 660 APETPDNITISREAQGEVPASDSKTECTAL 689
 Db 661 APETPDNITISREAQGEVPASDSKTECTAL 690

RESULT 5
 ABB12311
 ID ABB12311 standard; peptide; 700 AA.
 AC ABB12311;
 XX 11-JAN-2002 (first entry)
 XX Human Na-dependent phosphate transporter homologue, SEQ ID NO:2681.
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnerary; antiulcer.
 XX Homo sapiens.
 OS WO200157188-A2.
 PN 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US03800.
 XX 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 XX (HYSB-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-457740/49.
 DR N-PSDB; ABA09555.
 XX Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 FT e.g. arthritis and cancer -
 PS Claim 20; Page 329; 1963pp; English.
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.
 XX Sequence 700 AA;
 SQ
 Query Match 99.6%; Score 3581.5; DB 22; Length 700;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 688; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MAWPBLGDAQNPDKYLEGAGQQTAPDKSKETNK-NNTEAPVTKIELPSYSTATLI 59
 Db 11 MAWPBLGDAQNPDKYLEGAGQQTAPDKSKETNKTDNTEAPVTKIELPSYSTATLI 70
 QY 60 DEPTVEDDPPNLTLDQSGIKWSEKDTKGKILCFPGQIGRILLGLFLYFVCSLDILSS 119
 Db 71 DEPTVEDDPPNLTLDQSGIKWSEKDTKGKILCFPGQIGRILLGLFLYFVCSLDILSS 130
 QY 120 AFQIVGKAGQOFFSNSIMSNPLGLVIGLVTVLVVQSSSTSTSIYVSNVSSLLTVRA 179
 Db 131 AFQIVGKAGQOFFSNSIMSNPLGLVIGLVTVLVVQSSSTSTSIYVSNVSSLLTVRA 190
 QY 180 AIPIMGANIGTSINTIIVALMOVGDRSFRAPAGATVHDFNWLVLVLLPVEVATHY 239
 Db 191 AIPIMGANIGTSINTIIVALMOVGDRSFRAPAGATVHDFNWLVLVLLPVEVATHY 250
 QY 240 LEIITOLIVESPHFKNGEDAPDLLKVIPTKTLIVOLDKKVISOIAMNDEKAKNSLVK 299
 Db 251 LEIITOLIVESPHFKNGEDAPDLLKVIPTKTLIVOLDKKVISOIAMNDEKAKNSLVK 310
 QY 300 IWCKTFNKTQINVTVPSTANCTSPSLCWTGDIQNWTKNVTYKENTAKOHLFVNFHLP 359
 Db 311 IWCKTFNKTQINVTVPSTANCTSPSLCWTGDIQNWTKNVTYKENTAKOHLFVNFHLP 370
 QY 360 DLAVGTILLISLVLCOCLIMIVKILGSLVKGQVATVIKKTINTDPPPPFAWLGYLAI 419
 Db 371 DLAVGTILLISLVLCOCLIMIVKILGSLVKGQVATVIKKTINTDPPPPFAWLGYLAI 430
 QY 420 LVGAGMTFVQSSSVFTSALTPILGIVTIERAYPLTIGSNIGTITTTTALAALASPGNA 479
 Db 431 LVGAGMTFVQSSSVFTSALTPILGIVTIERAYPLTIGSNIGTITTTTALAALASPGNA 490
 QY 480 LRSLOIALCHFEFFNIGILLWYPIPTPLPRMAKGLGNISAKYRWFVYLIIFFFLI 539
 Db 491 LRSLOIALCHFEFFNIGILLWYPIPTPLPRMAKGLGNISAKYRWFVYLIIFFFLI 550
 QY 540 PLTVFGLSLAGRWLVGVGVVVFVIIILVCLRLQLQSCRPVLPKLIQNNWFLPMWSSL 599
 Db 551 PLTVFGLSLAGRWLVGVGVVVFVIIILVCLRLQLQSCRPVLPKLIQNNWFLPMWSSL 610
 QY 600 KPWDVAVSKFTGCEQWCCCRVCCACCLCGCPKCCCKCELEAEQAGQDVPYK 659
 Db 611 KPWDVAVSKFTGCEQWCCCRVCCACCLCGCPKCCCKCELEAEQAGQDVPYK 670
 QY 660 APETPDNITISREAQGEVPASDSKTECTAL 689

Db 671 APETFDNITISREAQGEVPASDSKTECTAL 700

RESULT 6
AAW79615
ID AAW79615 standard; Protein; 700 AA.
XX
AC AAW79615;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 3261.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
DR N-PSDB; AAK52748.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
XX Claim 20; Page 296-297; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAW80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX Sequence 700 AA;
SQ
Query Match 99.6%; Score 3581.5; DB 22; Length 700;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 688; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
1 MAPWPELGDAQPNPDKYLGAAGQOPTAPDKSKETNK-NNTPEAPVTKIELLPSTATLI 59
11 MAPWPELGDAQPNPDKYLGAAGQOPTAPDKSKETNKTDNTEAPVTKIELLPSTATLI 70

QY 60 DEPTVDDPNNLPTLQDSGIGKWSERDTGKILCFQGIQGRILILLGLFLYFFVCSLDILSS 119
DB 71 DEPTVDDPNNLPTLQDSGIGKWSERDTGKILCFQGIQGRILILLGLFLYFFVCSLDILSS 130
QY 120 AFOLVGKMGAGOFFSNSIMSNPLGLGIVGLVTVLVVSSSTSTSVVSVSSSLATVRA 179
DB 131 AFOLVGKMGAGOFFSNSIMSNPLGLGIVGLVTVLVVSSSTSTSVVSVSSSLATVRA 190
QY 180 AIPIMGANIGTSINTTIVALMQVGRSEFRFAFAGATVHDFFNWLSVLVLEVEVATHY 239
DB 191 AIPIMGANIGTSINTTIVALMQVGRSEFRFAFAGATVHDFFNWLSVLVLEVEVATHY 250
QY 240 LEIITOLIIVESHFKNGEDAPDLIKVITKPFKLIVOLDKKVISOIANDKAKNKSLYK 299
DB 251 LEIITOLIIVESHFKNGEDAPDLIKVITKPFKLIVOLDKKVISOIANDKAKNKSLYK 310
QY 300 IWCKTFTNKTQINVTVPSTANCTSPSLCWTGDIQNWTKMNTYKENTIAKQHIHFNHFLP 359
DB 311 IWCKTFTNKTQINVTVPSTANCTSPSLCWTGDIQNWTKMNTYKENTIAKQHIHFNHFLP 370
QY 360 DLAVGTILLISLLVLCGLIMIVKILGSLVKGOVATVTKTINTDPPFPFALTCYLAI 419
DB 371 DLAVGTILLISLLVLCGLIMIVKILGSLVKGOVATVTKTINTDPPFPFALTCYLAI 430
QY 420 LVGAGMTFVQSSSVFTSALTPLIGIVTIERAYPLTGSNIGTTTITAILAALASPGNA 479
DB 431 LVGAGMTFVQSSSVFTSALTPLIGIVTIERAYPLTGSNIGTTTITAILAALASPGNA 490
QY 480 LRSLQIALCHEFFNISGILLNWPDPFTRPIMAKGLGNISAKYRNFVYLIIFFFLI 539
DB 491 LRSLQIALCHEFFNISGILLNWPDPFTRPIMAKGLGNISAKYRNFVYLIIFFFLI 550
QY 540 PLTVFGLSLAGWRVLVGVVPVFIILVLCRLQLQSRCPVLPKLONNFPLMWRSL 599
DB 551 PLTVFGLSLAGWRVLVGVVPVFIILVLCRLQLQSRCPVLPKLONNFPLMWRSL 610
QY 600 KPWDVAVSKFTGCFOMRCCCCVCCRACTLCGCKCCKCCEDLEAORSGODVPVK 659
DB 611 KPWDVAVSKFTGCFOMRCCCCVCCRACTLCGCKCCKCCEDLEAORSGODVPVK 670
QY 660 APETFDNITISREAQGEVPASDSKTECTAL 689
DB 671 APETFDNITISREAQGEVPASDSKTECTAL 700

RESULT 7.
AAW77414
ID AAW77414 standard; Protein; 690 AA.
XX
AC AAW77414;
XX
DT 02-FEB-1999 (first entry)
XX Human sodium dependent phosphate transporter IPT-1.
DE
XX IPT-1; sodium dependent phosphate transporter; human;
KW kidney failure; kidney disease; uraemic bone disease; cancer;
KW diagnosis; therapy; vaccine.
XX
XX Homo sapiens.
OS
XX
PN EP875569-A1.
XX
XX 04-NOV-1998.
PD
XX
XX 09-APR-1998; 98EP-0302815.
XX
XX 23-SEP-1997; 97US-0935433.
PR
XX 28-APR-1997; 97US-0044974.
PR
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX

PI Feild J;
XX WPI; 1998-559435/48.
DR N-PSDB; RAV77414.
XX
PT New DNA encoding sodium-dependent phosphate transporter protein
PT IPT-1 - used to prevent, treat and diagnose e.g. chronic renal
PT failure, end-stage renal disease, uraemic bone disease and cancer
XX
XX Claim 1; Page 17-19; 24pp; English.
XX
CC This is the amino acid sequence of human sodium dependent phosphate
CC transporter IPT-1, as deduced from the nucleotide sequence of a
CC cDNA clone (see XAV59498). It shows about 76% identity in 691 amino
CC acids with bovine sodium dependent phosphate transporter and 55%
CC identity in 625 amino acids with human Napi-3. Methods are
CC provided for the production of IPT-1 polypeptides in recombinant
CC host cells. Such polypeptides can be used to raise antibodies and
CC also in a claimed method for identifying compounds which inhibit or
CC agonise the IPT-1 polypeptide. Agonists can be used to treat a
CC subject in need of enhanced activity or expression of IPT-1, while
CC antagonists can be used to treat a subject having need to inhibit
CC activity or expression of IPT-1. A claimed process for diagnosing
CC a disease or susceptibility to disease related to IPT-1 expression
CC or activity involves analysing for the presence or amount of IPT-1
CC expression in a sample. IPT-1 polypeptides and polynucleotides can
CC be used for prevention, treatment and diagnosis of e.g. chronic
CC renal failure, end-stage renal disease, uraemic bone disease and
CC cancer.
XX
XX Sequence 690 AA;
SQ
Query Match 99.3%; Score 3570.5; DB 19; Length 690;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 687; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 MAPWELGDAQNPDKYLEGAGQOPTAPDKSKETNK-NNTEAPVTKIELPSYSTATLI 59
Db 1 MAPWELGDAQNPDKYLEGAGQOPTAPDKSKETNKNTDTEAPVTKIELPSYSTATLI 60
QY 60 DEPTVEDDNNPTLQDSGIKWSERDTKGLICFFGIGRLILIGLTFYFVCSLDLSS 119
Db 61 DEPTVEDDNNPTLQDSGIKWSERDTKGLICFFGIGRLILIGLTFYFVCSLDLSS 120
QY 120 AFQLVCKWAGOFFNSNSIMNPLGLVIGLVTVLVQSSSTSTSIIVVSWSSLLTVRA 179
Db 121 AFQLVCKWAGOFFNSNSIMNPLGLVIGLVTVLVQSSSTSTSIIVVSWSSLLTVRA 180
QY 180 AIPFINGANIGTSITNTIVALMQVDSRFRAPAGATVHDFFNWLSVLVLLPVEVATHY 239
Db 181 AIPFINGANIGTSITNTIVALMQVDSRFRAPAGATVHDFFNWLSVLVLLPVEVATHY 240
QY 240 LEIITQILVESHFKNGEDADLAKVITKPTKLIIVOLDKKVISOIANDKAKNSLYK 299
Db 241 LEIITQILVESHFKNGEDADLAKVITKPTKLIIVOLDKKVISOIANDKAKNSLYK 300
QY 300 IWCKTNTKNTQNVTPSTANTCSPSLCWDGIGQWNTKNTYKENTAKQHLFVNFHLP 359
Db 301 IWCKTNTKNTQNVTPSTANTCSPSLCWDGIGQWNTKNTYKENTAKQHLFVNFHLP 360
QY 360 DLAVGTILILSLVLCGLIMVILKGLSVLKGQVATVTKTINTDPPFPFAMLTGYLAI 419
Db 361 DLAVGTILILSLVLCGLIMVILKGLSVLKGQVATVTKTINTDPPFPFAMLTGYLAI 420
QY 420 LVGAGMTFIVQSSVFTSALTPLIGIVITIERAYPLTIGSNIGTITTAIALAPGNA 479
Db 421 LVGAGMTFIVQSSVFTSALTPLIGIVITIERAYPLTIGSNIGTITTAIALAPGNA 480
QY 480 LRSLQIALCHFFFNISGILLWYIPTRPIRMAGLGNISAKYRFAFYLLIIEFFLI 539
Db 481 LRSLQIALCHFFFNISGILLWYIPTRPIRMAGLGNISAKYRFAFYLLIIEFFLI 540
QY 540 PLTVFGLSLAGWRVLVGVGVVVFIIILVLCLELQSRCPVLPKQLQNNFLELWMSL 599

Db 541 PLTVFGLSLAGWRVLVGVGVVVFIIILVLCLELQSRCPVLPKQLQNNFLELWMSL 600
QY 600 KPWDVAVSKFTGCFQMRCCGCCVCCACLLCGCPKCCRCCKCEDLBEAOGQDVPVK 659
Db 601 KPWDVAVSKFTGCFQMRCCGCCVCCACLLCGCPKCCRCCKCEDLBEAOGQDVPVK 660
QY 660 APPTFDNITISREAGVGPASDSKTECTAL 689
Db 661 APPTFDNITISREAGVGPASDSKTECTAL 690
RESULT 8
AM93865
ID AM93865 standard; Protein; 631 AA.
XX AM93865;
AC AM93865;
XX
DT 06-NOV-2001 (first entry)
XX Human polypeptide, SEQ ID NO: 3967.
DR Human; full length cDNA; cDNA synthesis; oligo-capping.
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX Homo sapiens.
OS
XX EP1130094-A2.
PN
XX
PD 05-SEP-2001.
XX
XX 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
XX (HELI-) HELIX RES INST.
PI Ota T. Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX WPI; 2001-52455/58.
DR N-PSDB; AAK94823.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
XX Claim 8; SEQ ID NO 3967; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a polypeptide
CC encoded by a full length human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 631 AA;
Query Match 90.1%; Score 3240; DB 22; Length 631;
Best Local Similarity 91.2%; Pred. No. 1.3e-301;
Matches 629; Conservative 1; Mismatches 0; Indels 60; Gaps 2;
QY 1 MAPWELGDAQNPDKYLEGAGQOPTAPDKSKETNK-NNTEAPVTKIELPSYSTATLI 59
Db 1 MAPWELGDAQNPDKYLEGAGQOPTAPDKSKETNKNTDTEAPVTKIELPSYSTATLI 60
QY 60 DEPTVEDDNNPTLQDSGIKWSERDTKGLICFFGIGRLILIGLTFYFVCSLDLSS 119

Db 61 DEPTVEDDNNLPTLQDSGIKWSERDTKGKILCFGGIGKLLILGLFLYFVCSLDILSS 120
QY 120 AFQLVGKMGAGQFFNSSTMSNPLGLVIGVATVVLVQSSSTSTSIIVSMVSSSLITVRA 179
Db 121 AFQLVGKMGAGQFFNSSTMSNPLGLVIGVATVVLVQSSSTSTSIIVSMVSSSLITVRA 180
QY 180 AIPIMGANIGTSITNTIIVAMQVCDRSEPRRAFAGATVHDFNMLSVLVLPEVATHY 239
Db 181 AIPIMGANIGTSITNTIIVAMQVCDRSEPRRAFAGATVHDFNMLSVLVLPEVATHY 240
QY 240 LEITQILVSEHFHNGEDAPDLKVTPTKLIIVOLDKXVISOIAMNDEKAKNSLVK 299
Db 241 LEITQILVSEHFHNGEDAPDLKVTPTKLIIVOLDKXVISOIAMNDEKAKNSLVK 300
QY 300 IWCKTFNKTQINVTVPSTACTSPSLCWTGDTQNTMKNVTYKENIAKQHFVNPHLP 359
Db 301 IWCKTFNKTQINVTVPSTACTSPSLCWTGDTQNTMKNVTYKENIAKQHFVNPHLP 360
QY 360 DLAVGTILAILLSLLVLCGLIMIVKILGSLVKGQVATVIKKTINTDPPFPFAMLTGYLAI 419
Db 361 DLAVGTILAILLSLLVLCGLIMIVKILGSLVKGQVATVIKKTINTDPPFPFAMLTGYLAI 420
QY 420 LVGAGWTFIVQSSSVFTSALTPLIGIGVITIERAYPLTGLSGNIGTTTTLAALASFGNA 479
Db 421 LVGAGWTFIVQSSSVFTSALTPLIGIGVITIERAYPLTGLSGNIGTTTTLAALASFGNA 480
QY 480 LRSLQLALCHFFNFISGILLWYPIPTPLPIRWAKGLGNISAKYRFAVEYLIIPFLLI 539
Db 459 -----LGNISAKYRFAVEYLIIPFLLI 481
QY 540 PLTVFGLSLAGWRLVGVGVVVFIIILVLCRLLOSRCPRLPKLQNNWFLPLMWSL 599
Db 482 PLTVFGLSLAGWRLVGVGVVVFIIILVLCRLLOSRCPRLPKLQNNWFLPLMWSL 541
QY 600 KPMDAVVSKFTGCFQMRCCCRVCCACCLCGCPKCCCKCEDLEEAQEGQDVVK 659
Db 542 KPMDAVVSKFTGCFQMRCCCRVCCACCLCGCPKCCCKCEDLEEAQEGQDVVK 601
QY 660 APETFDNITISREAGQEVPSDSKTECTAL 689
Db 602 APETFDNITISREAGQEVPSDSKTECTAL 631

RESULT 9
AA06591
ID AA06591 standard; Protein; 397 AA.

XX AC AA06591;

XX DT 06-NOV-2001 (first entry)

XX DE Human polypeptide, SEQ ID NO: 3955.

XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX OS Homo sapiens.

XX PN EP1130094-A2.

XX PD 05-SEP-2001.

XX PF 07-JUL-2000; 2000EP-0114089.

XX PR 08-JUL-1999; 99JP-0194486.

XX PR 11-JAN-2000; 2000JP-0118774.

XX PR 02-MAY-2000; 2000JP-0183765.

XX PA (HELI-) HELIX RES INST.

XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

XX FI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX X

DR WPI; 2001-524255/58.
DR N-PSDB; AAK94816.
XX 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Claim 8; SEQ ID NO 3955; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a polypeptide
CC encoded by a full length human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 397 AA;

Query Match 58.3%; Score 2098; DB 22; Length 397;

Best Local Similarity 98.3%; Pred. No. 2.8e-192;

Matches 396; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 287 MNDEKAKNSLVKIWKCTFTNKTQINVTVPSTACTSPSLCWTGQINWTKNVTYKENI 346

Db 1 MNDEKAKNSLVKIWKCTFTNKTQINVTVPSTACTSPSLCWTGQINWTKNVTYKENI 60

QY 347 AKQHLFVNPHLPDLAVGTILAILLSLLVLCGLIMIVKILGSLVKGQVATVIKKTINTDP 406

Db 61 AKQHLFVNPHLPDLAVGTILAILLSLLVLCGLIMIVKILGSLVKGQVATVIKKTINTDP 120

QY 407 PFPFAMLTGYLAILVAGWTFIVQSSSVFTSALTPLIGIGVITIERAYPLTGLSGNIGTTT 466

Db 121. PFPFAMLTGYLAILVAGWTFIVQSSSVFTSALTPLIGIGVITIERAYPLTGLSGNIGTTT 180

QY 467 TAILAALASFGNALRSSLOIALCHFFNFISGILLWYPIPTPLPIRWAKGLGNISAKYRW 526

Db 181 TAILAALASFGNALRSSLOIALCHFFNFISGILLWYPIPTPLPIRWAKGLGNISAKYRW 240

QY 527 FAVFYLIIFPFLIPLTVFGLSLAGWRLVGVGVVVFIIILVLCRLLOSRCPRLPKL 586

Db 241 FAVFYLIIFPFLIPLTVFGLSLAGWRLVGVGVVVFIIILVLCRLLOSRCPRLPKL 300

QY 587 QNWNFLPLMWSRLKPMDAVVSKFTGCFQMRCCCRVCCACCLCGCPKCCCKCED 646

Db 301 QN-----NWSRLKPMDAVVSKFTGCFQMRCCCRVCCACCLCGCPKCCCKCED 354

QY 647 LEEAQEGQDVVKAPETFDNITISREAGQEVPSDSKTECTAL 689

Db 355 LEEAQEGQDVVKAPETFDNITISREAGQEVPSDSKTECTAL 397

RESULT 10

AA06591

ID AA06591 standard; Protein; 599 AA.

XX AC AA06591;

XX DT 25-SEP-2001 (first entry)

XX DE Human protein having hydrophobic domain, HP03878.

XX KW Human; hydrophobic domain; gene therapy; nutritional supplement;
XX cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
XX multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
XX haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
XX Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
XX haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
XX contraceptive; antiinfertility; antiinflammatory.

XX WO200100805-A2.
 PN 04-JAN-2001.
 XX 23-JUN-2000; 2000WO-IB00926.
 XX 25-JUN-1999; 99US-0141031.
 XX 08-JUL-1999; 99DE-1031454.
 XX 08-JUL-1999; 99DE-1031478.
 XX 08-JUL-1999; 99DE-1031563.
 XX 09-JUL-1999; 99DE-1032122.
 XX 09-JUL-1999; 99DE-1032124.
 XX 09-JUL-1999; 99DE-1032125.
 XX 09-JUL-1999; 99DE-1032128.
 XX 09-JUL-1999; 99DE-1032180.
 XX 09-JUL-1999; 99DE-1032182.
 XX 09-JUL-1999; 99DE-1032190.
 XX 09-JUL-1999; 99DE-1032191.
 XX 09-JUL-1999; 99DE-1032209.
 XX 09-JUL-1999; 99DE-1032212.
 XX 09-JUL-1999; 99DE-1032227.
 XX 09-JUL-1999; 99DE-1032228.
 XX 09-JUL-1999; 99DE-1032229.
 XX 09-JUL-1999; 99DE-1032230.
 XX 14-JUL-1999; 99DE-1032927.
 XX 14-JUL-1999; 99DE-1033005.
 XX 14-JUL-1999; 99DE-1033006.
 XX 27-AUG-1999; 99DE-1040764.
 XX 27-AUG-1999; 99DE-1040765.
 XX 27-AUG-1999; 99DE-1040766.
 XX 27-AUG-1999; 99DE-1040830.
 XX 27-AUG-1999; 99DE-1040831.
 XX 27-AUG-1999; 99DE-1040832.
 XX 27-AUG-1999; 99DE-1040833.
 XX 31-AUG-1999; 99DE-1041378.
 XX 31-AUG-1999; 99DE-1041379.
 XX 31-AUG-1999; 99DE-1041395.
 XX 03-SEP-1999; 99DE-1042077.
 XX 03-SEP-1999; 99DE-1042078.
 XX 03-SEP-1999; 99DE-1042079.
 XX 03-SEP-1999; 99DE-1042088.
 XX (BADI) BASF AG.
 XX Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
 XX WPI; 2001-071486/08.
 XX N-PSDB; AAF67998.
 XX Corynebacterium glutamicum nucleic acids encoding membrane construction
 PT and membrane transport proteins or their portions, useful for typing or
 PT identifying C. glutamicum or related bacteria, and as markers for
 PT transformation -
 XX Claim 20; Page 876-877; 1119pp; English.
 XX AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane
 CC construction and membrane transport (MCT) proteins given in AAF76510 to
 CC AAB76847. The MCT nucleic acids and proteins are useful in the
 CC identification of microorganisms which can be used to produce fine
 CC chemicals, for modulating fine chemical production in C. glutamicum or
 CC related bacteria (e.g. Brevibacterium lactofermentum), the typing or
 CC identification of C. glutamicum or related bacteria, as reference points
 CC for mapping C. glutamicum genome, and as markers for transformation.
 CC AAF68082 and AAF68082 represent sequencing primers which are used in an
 CC example from the present invention.
 XX Sequence 411 AA;
 SQ Query Watch 11.4%; Score 410; DB 22; Length 411;
 Best Local Similarity 27.6%; Pred. No. 3e-30;
 Matches 120; Conservative 77; Mismatches 152; Indels 86; Gaps 8;

QY 101 ILLGLYFFVCSLDILSSAFOIVGKVA-----CQFENS--SIMSNPLGIVGLV 151
 DB 49 VILSGWGFVRWLEVLISIIIGINILIDGVGFSTFTQMVQVAKDPLIGVLIGIL 108
 QY 152 VTLVQSSSTSTSVYSWSSSLTVRAAIPIMGANIGTSINTIVALMOYGDORSFRR 211
 DB 109 ATALVQSSSTTTTITVTANGTGVSPVAIPILGANIGTTITAMINAFSVYGERREFR 168
 QY 212 APAGATVHDFFNWLVSULLPVEVATHYLEITOLIVESHFHNGEDAP--DLLKVITKP 269
 DB 169 AFTVAAMHVNENLVILVLFVVELLFHFRITSGAIATEITLTGSLFTSGWTKIFDP 228
 QY 270 FTKLIVQLDKVLSQIAMNDEKAKNKSIVKWKCTFTNKTIQINVTVPSTANCTSPSLCWT 329
 DB 229 PTQLIGM--NGLIGSIG-----NPSISAIVC----- 252
 QY 330 DGIQNTMKNVTYKENIAKQOHIFVNPHLPDLAVGTILLILSLVLCGLIMVKILGSV 389
 DB 253 -----LVGTILLISVRAMS-----SQRTI 274
 QY 390 LKGQVATVTKTINTDPPFPFAMLTGYLAILVGAGMTFIVOSSSVFTSALTLLIGIGVIT 449
 DB 275 TAAVTSTINDKVINPENSFKATILSNFSLVGLFTIMVTASSVTVASNQVPAASGVVK 334
 QY 450 IERAYPLTGSNIGTTTTTALALASPGRNLRSLQIALCHFFFNISGILLWYPIF-FTR 508
 DB 335 QKPLLGVLIGANVGTTTAMFATFAIVSDQGEFAIQALHLIVNFTGALLVLCIPQLAN 394
 QY 509 LPIRMAGLGNISAK 523
 DB 395 VIIHLAERTANLTAR 409
 RESULT 14
 ABP29511
 ID ABP29511 standard; Protein; 549 AA.
 XX AC ABP29511;
 XX DT 02-JUL-2002 (first entry)
 XX Streptococcus polypeptide SEQ ID NO 8198.
 DE Streptococcus
 KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX Streptococcus pyogenes.
 XX WO200234771-A2.
 XX 02-MAY-2002.
 XX 29-OCT-2001; 2001WO-GB04789.
 XX 27-OCT-2000; 2000GB-0026333.
 XX 24-NOV-2000; 2000GB-0028727.
 XX 07-MAR-2001; 2001GB-0005640.
 XX (CHIR-) CHIRON SPA.
 XX (GENO-) INST GENOMIC RES.
 PI Telford J, Massignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 XX WPI; 2002-352536/38.
 DR N-PSDB; ABN70142.
 XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 XX for detecting a compound that binds to the protein -

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2003, 15:48:07 ; Search time 49 Seconds
(without alignments)
1352.249 Million cell updates/sec

Title: US-10-052-664-1
Perfect score: 3597
Sequence: 1 MAPWELGDAQNDPKYLEG.....SREAGQGVASDSKTECTAL 689

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2851	79.3	693	2 S49228	sodium-dependent p
2	1721	47.8	637	2 A48189	sodium/phosphate c
3	1706.5	47.4	853	2 A54366	sodium/phosphate c
4	1698.5	47.2	639	2 B48189	sodium/phosphate c
5	1682	46.8	637	2 A54000	sodium/phosphate c
6	1681.5	46.7	642	2 I46534	renal sodium-depen
7	732.5	20.4	504	2 T27914	hypothetical prote
8	559.5	15.6	382	2 D82295	nptA protein VC067
9	283	7.9	555	2 D89770	conserved hypothet
10	274.5	7.6	544	2 AB1178	transport protein
11	264.5	7.3	543	2 E95057	Na/Pi cotransporte
12	262.5	7.3	543	2 G97926	conserved hypothet
13	247.5	6.9	543	2 G83825	hypothetical prote
14	242.5	6.7	569	2 E90554	conserved hypothet
15	218.5	6.1	593	2 H71283	conserved hypothet
16	203	5.6	310	2 F69952	Na+/Pi cotransport
17	194.5	5.4	310	2 A83819	hypothetical prote
18	179	5.0	253	2 AF1535	transport protein
19	165	4.6	543	2 C65209	hypothetical 59.5
20	161	4.5	543	2 B91246	probable alpha hel
21	161	4.5	543	2 H86093	probable alpha hel
22	146.5	4.1	441	2 AB1542	PTS system, Lichen
23	146.5	4.1	682	2 AG3351	transporter EMB107
24	146	4.1	582	2 C82961	conserved hypothet
25	145.5	4.0	543	2 AI1011	probable membrane
26	142.5	4.0	441	2 AD1184	PTS system, Lichen
27	139.5	3.9	550	2 AD2852	Na+/Pi-cotransport
28	139.5	3.9	555	2 B97629	hypothetical prote
29	139.5	3.9	630	2 T38110	major facilitator

amino acid transpo
magnesium citrate
hypothetical prote
spoVB related memb
hypothetical prote
hypothetical prote
periplasmic phosph
cytochrome-c oxida
cytochrome-c oxida
L-lactate permease
membrane protein
conserved hypothet
NADH2 dehydrogenas
SNG1 protein - yea
hypothetical prote

30 136 3.8 520 2 H90447
31 135.5 3.8 442 2 A83743
32 133.5 3.7 443 2 AG1335
33 132.5 3.7 539 2 E97025
34 131 3.6 164 2 T24272
35 129 3.6 152 2 T18975
36 129 3.6 654 2 E64245
37 128 3.6 188 2 T15651
38 128 3.6 511 2 T11467
39 128 3.6 513 2 T13782
40 127.5 3.5 524 2 H84141
41 126.5 3.5 307 2 B95099
42 126.5 3.5 307 2 A97967
43 126.5 3.5 498 2 T14236
44 125 3.5 547 2 B53920
45 124.5 3.5 456 2 B90069

ALIGNMENTS

RESULT 1
S49228
C:Species: Bos primigenius taurus - bovine
C:Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 05-Nov-1999
C:Accession: S68972, S49228
R:Helps, C.; Murer, H.; McGivan, J.
Eur. J. Biochem. 228, 927-930, 1995
A:Title: Cloning, sequence analysis and expression of the cDNA encoding a sodium-depende
A:Reference number: S68972; MUID:95255303; PMID:7737195
A:Accession: S68972
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-693 <HE2>
A:Cross-references: EMBL:X81699; NID:G547483; PIDN:CAA57345.1; PID:G547484

Query Match 79.3%; Score 2851; DB 2; Length 693;
Best Local Similarity 76.3%; Pred. No. 1.1e-193;
Matches 531; Conservative 82; Mismatches 73; Indels 10; Gaps 3;

QY	1	MAPWELGDAQNDPKYLEGAAQOQPTAPDKSKTNQNTNRAFPVTKIELLPSYSTATLID 60
DB	1	MAPWELGDAQNDPKYLEGAAQOQPTAPDKSKTNQNTNRAFPVTKIELLPSYSTATLIE 60
QY	61	EPTVEDDPMNLPTLOSGIKWSEKTKKILCFQGIKRLILLGLAYFVCSLDLSSA 120
DB	61	EPTVEDDPMNLPTLOSGIKWSEKTKKILCFQGIKRLILLGLAYFVCSLDLSSA 120
QY	121	FOLVGGKAGOFFFNSNSINPLAGLIVGLVTLVQSSSTSTSIWVSWSLLTVRAA 180
DB	121	FOLVGGKAGOFFFNSNSINPLAGLIVGLVTLVQSSSTSTSIWVSWSLLTVRAA 180
QY	181	IPITMGANIGTSINTTIVAMQVDSFRAPAGATVHDFNNLSVLVLLPEVATHYL 240
DB	181	IPITMGANIGTSINTTIVAMQVDSFRAPAGATVHDFNNLSVLVLLPEVATGYL 240
QY	241	ELITOLIVESHFHNGSDAPDLKLVTKPFTKLIVOLDKKVISOIAMNDEKAKKSLVKI 300
DB	241	ELITOLIVESHFHNGSDAPDLKLVTKPFTKLIVOLDKKVISOIAMNDESVQKWSMKI 300
QY	301	WCKTPTNKTQINVTVPSTANTSPSLCWTDDGIQNWTKMNTYKENIAKQHFVNFHLPD 360
DB	301	WCKTPTNVTNVTVPSPENCTSPSLCWTDDGLYTWTKNTYKENIAKQHFVNFNLS 360
QY	361	LAVGTHAILSLVLCCLIMVKILGSLVAGVATVTKTINTDTPPPPAWLTCYLAIL 420
DB	361	AVGTHAILSLVLCCLILVILGSLVAGVATVTKTINTDTPPPPAWLTCYLAIL 420
QY	421	VGAGMTFTVQSSSVFTSALTPLIGITVITIRAYPLTLGSGNIGTITTAALASPGNAL 480
DB	421	VGAGMTFTVQSSSVFTSALTPLIGITVITIRAYPLTLGSGNIGTITTAALASPGSTL 480


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Db 214 TDFRAAGATVDCFNWLSVLVLLPLEAATGYLHHVTGLVWASFNIRGGSDAPDLIKTI 273
QY 267 TKPTKLIIVOLDKXVISOIAMDENAKXKSLVWKIWKCTFTNKQTQINVTVPSTANCSPSL 326
Db 274 TEPFKLIQDLSVTSIATDESRNHSIRIWRCHRDPEASTSMARAST-----NI 327
QY 327 CWTGICQNMWKNVYKENIAKCOHIFVNPHLPDLAVGTITLILSLVLCCLIMVKIL 386
Db 328 SETHG--NATWE-----KCNHIFVDTQPLDPLAVGLILLAGSLVLCITLILVWML 376
QY 387 GSVLKGVATVTKTINTDPPPPFAWLGTYLAILVGMFTFVQSSSVFTSALTPLIGIG 446
Db 377 NSLLKGVQAKVIQKVINOTDLPAPTWTGYPAMVGAAMTFVQSSSVFTSALTPLVGLG 436
QY 447 VITIERAYPLTGSNIGTITTAIALASPGNALRSSLOIALCHPFFNISGILWYPIFP 506
Db 437 VISIERAYPLTGSNIGTITTAIALASPGNALRSSLOIALCHPFFNISGILWYELPC 496
QY 507 TELPIRMAGLGNISAKYEFVAVFYLIIFPLIPLTVFGLSLAGRWLVGVGVVWFII 566
Db 497 TELPIRMAGLGNISAKYEFVAVFYLIIFPLIPLTVFGLSLAGRWLVGVGVVWFII 566
QY 567 LVLCRLRQRCRPLPKLQNNFPLWMSLKPMDVAVSKFTGCFQMRCCCCCR 622
Db 557 FVLINVLQSRSPRLPKLQNNFPLWMSLKPMDVAVSKFTGCFQMRCCCCCR 622
Db 557 FVLINVLQSRSPRLPKLQNNFPLWMSLKPMDVAVSKFTGCFQMRCCCCCR 605

RESULT 7
T27914
hypothetical protein ZK563.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27914
R;ie, T.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid ZK563.
A;Reference number: Z20439
A;Accession: T27914
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-504 <LET>
A;Cross-references: EMBL:U40061; PIDN:AAA81148.1; CESP:ZK563.2
C;Genetics:
A;Gene: CESP:ZK563.2
A;Introns: 20/2; 47/1; 94/1; 138/1; 239/3; 275/3; 329/2; 371/3; 423/3

Query Match 20.4%; Score 732.5; DB 2; Length 504;
Best Local Similarity 30.0%; Pred. No. 3.9e-44;
Matches 166; Conservative 110; Mismatches 148; Indels 129; Gaps 7;
QY 65 VDDPNNLPTLQDGIKWSRDTKGLCFQGIKRLILGLYFFVCSLDILGSAPOLV 124
Db 29 VGDTEPAHKGLIISWTPTPKHKVYIYCSFLIILILVLYFVCSLANMTAGLL 88
QY 125 GKMGAGQFFNSIMNPLGLVIGLVTVLVQSSSTSTSVVSWSSSLTVRAAPIII 184
Db 89 GSRGLGKAIQESPLINDPISAVVGMATVVLQSAITTTNLTVMVAAMITVHDAIPVM 148
QY 185 MGANIGSINTVVALMQVDRSEFRAPAGATVHDFPNWLVLLPVVATVYLIIT 244
Db 149 IGSELGSLVNAVMSLAYSGKEQFRAPASAIIGDFVNCGLFVIFPMEMFTGLIEKVS 208
QY 245 QLVIESHFKNGEDAPDLAKVITKPTKLIIVOLDKXVISOIAMDENAKXKSLVWKI 304
Db 209 WIVDPLISEGLSF-KYLELITDPIQVILQ----- 239
QY 305 FNNKQINVTVPSTANCSPSLCWTGDIQNMWKNVYKENIAKCOHIFVNPHLPDLAVG 364
Db 240 ----- 239
QY 365 TILLILSLVLCGLIMVKILGSLVKGQVATVTKTINTDPPPPFAMLTGYLAILVAG 424

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Db 240 -----KLLDGHAAVYRNLLSKQCPGMWKPCTGYLVMLVG-- 274
QY 425 MTFIVOSSVFTSALTPLIGVITIERAYPLTGLSNIGTITTAIALASPGNALRSSL 484
Db 275 ---LIOSNIFSSSLTPVGGVITLQMPVPLVIGSNIGTITFSGVLAFAFSTDSRFEKAL 331
QY 485 QIALCHFFNINISGILLWYPIPTFR-LPIRMAGLGNISAKYEFVAVFYLIIFPLIPLTV 543
Db 332 HMANCQVINYIIGTCLFIVFCIKFVLSKGLGVITHYRNIVFVISTVLIIPFTI 391
QY 544 FGLSLAGRWLVGVGVVVFVFIILVLCR-----LQSSCRPLVPKLQNNFPLWMS 598
Db 392 IGLTLLPDNVIV-----IVFIILIIATCCFTICVLQNSCKEFLPKILHNSWFLPWMS 446
QY 599 LKPMDAVSK-FT 610
Db 447 LQYDPMCKVFT 459

RESULT 8
D82295
npA protein VC0676 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: D82295
R;Reidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82295
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-382 <HBI>
A;Cross-references: GB:AE004153; GB:AE003852; NID:ig9655103; PIDN:AAF93841.1; GSPDB:GN00.
A;Experimental source: serogroup O1; strain N16961; biotype H1 Tor
C;Genetics:
A;Gene: VC0676
A;Map position: 1

Query Match 15.6%; Score 559.5; DB 2; Length 382;
Best Local Similarity 30.7%; Pred. No. 4.9e-32;
Matches 152; Conservative 83; Mismatches 141; Indels 119; Gaps 12;
QY 58 LIDEPTEVDDPNNLPTLQDGIKWSRDTKGLCFQGIKRLILGLYFFVCSLDIL 117
Db 1 MINQATSPAPISLTT---KGLRWAN-----LAPMLLILLAVAV 38
QY 118 SSAPQLVGGKMGAGQFFNSIMNPLGLVIGLVTVLVQSSSTSTSVVSWSSSLTV 177
Db 39 GSGFKWATGDAQVLF---EPASHPIAGLMIGLVATALIQQSSSTVTSIIVGLVAGG-LPV 94
QY 178 RAAPITMGANTGTSITVITVALMQVDRSEFRAPAGATVHDFPNWLVLLPVVAT 237
Db 95 ETALPMWGMANTGTTVTNLTLSLGHMKKEEFRAFASATIHDFNLAFLVLIPLFEMMF 154
QY 238 HYLIIITOLIVSFHFKNGEDAP---DLLAKVITKPTKLIIVOLDKXVISOIAMDENAKN 294
Db 155 GILKSHMLVSLP-LATGDSMKMGDFIPIKTP-----VITGL----- 193
QY 295 KSLVKIWKCTFTNKQINVTVPSTANCSPSLCWTGDIQNMWKNVYKENIAKCOHIFV 354
Db 194 -----ETQLSV----- 199
QY 355 NFHLPLDVLAVGTITLILSLVLCGLIMVKILGSLVKGQVATVTKTINTDPPPPFAMLT 414
Db 200 ---LGNTFGVALIVLGATTFVATVWGMKSLMVGSGAREILQNAIG-----R 246
QY 415 GYL-AIILGAGMTFVQSSSVFTSALTPLIGVITIERAYPLTGLSNIGTITTAIALA 473
Db 247 GPLHGIASGTVTVLVQSSSTTTSLAVPLVGSGLVKLREIYPTFLGANIGTITTAIALA 306

```

R; Glaser, P.; Prangeul, L.; Buchrieser, C.; Anand, A.; Baquero, F.; Berche, P.; Bloechel, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Ettian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001

A; Authors: Kraft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Meak, C.; Schlucter, T.; Simoes, N.; Tarré, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria species*.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Accession: AB1178

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-544 <GLA>

A; Cross-references: GB|NC_003210; PID:CAC98904.1; PID:g16410215; GSPDB:GN00177

A; Experimental source: strain EGD-e

C; Genetics:

A; Gene: lmo0826

Query Match 7.6%; Score 274.5; DB 2; Length 544;
Best Local Similarity 22.6%; Pred. No. 9.9e-12;
Matches 108; Conservative 52; Mismatches 115; Indels 203; Gaps 13;

QY 94 FQIGRL-ILLAGFLYFFVCSLDTLSSAFOLVGKMGAGOFFSNSSIMNSPLGLGLVGLV 152
Db 11 FQIGGLGLFLGIKI-----MGDGLQMAAGRLRLDLDKYT--TNPFGVLAGILV 60

QY 153 TVLVQSSSTSTSVVSMVSSLLTVRAAIPPIINGANIGTSTINTVALMGQDRSEFRRA 212
Db 61 TVLIQSSSGTTLTVGLVSAFGMTLQAIGVINGANIGTTVTAIIG-----107

QY 213 PAGTVHDFNMLSVLVLLPVEVATHLEILLQLIVESHFGNGEDAPDLLKVIYFPYK 272
Db 108 -----IKLSEYSLPIIIVAGVALLFFPKN-----130

QY 273 LVLQDKKVISQIAMDSEKAKNSLVKIWCKTFNKTQINVTVPSTANTCPSLCWTDGI 332
Db 131 -----HKVKN-----135

QY 333 QNWTKMNTYKENIAKQOHIFVNFPLDPLAVGTILLLSLVLCGLIMIVKILGSVLK- 391
Db 136 -----IGQVFFG-----GALFYGLDLMGQMKP 159

QY 392 -----GQVATVTKTINDTPFFPAMLTGVLAILVAGAGTIVQSSVFTSALT 440
Db 160 LAGMSFHELTQNST-----NPFLLGLITFTTAVVQSSATIGILQ 202

QY 441 PLIGIGVITIERAYPLTIGSNIGTTTATLALAGPVALRSSLIQALCHFFFNIGILL 500
Db 203 ELVQGAIDLQALPVLFDNIGITTTAVLALAGSVAKRA----RATVFNILGAIL 258

QY 501 WYPI--PFTRL-----PIRMAGLGNISAKY--RWFVAYFLIILFFPL 540
Db 259 FMLILPFTSLAVYLGQMGFLNPMTIYVAGHFNITWTFIQFVIGAFAMVTKLIP 316

RESULT 11

E95057.

Na/Pi cotransporter II-related protein SP0496 [imported] - Streptococcus pneumoniae (str E95057).

C; Species: Streptococcus pneumoniae

C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C; Accession: E95057

C; Retention: H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heickson, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001

A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.

A; Reference number: A95000; MUID:21357209; PMID:11463916

A; Accession: E95057

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-543 <KUR>

A; Cross-references: GB|AE005672; PID:NAAK74654.1; PID:g14971968; GSPDB:GN00164; TIGR:SP. A; Experimental source: strain TIGR4

C:Genetics:
A:Gene: SP0496

Query Match 7.3%; Score 263.5; DB 2; Length 543;
Best Local Similarity 22.5%; Pred. No. 5.9e-11;
Matches 108; Conservative 53; Mismatches 134; Indels 185; Gaps 14;

QY 79 IKWSEDTKGLICFFQGGIGRLILLGLFYFFVCSLDILSSAFQVGVKAGOFFNSIS 138
DB 3 INWQE-----ILFHF-----LGLGLFYISIKNGDGLQQAADRLR--FYIDKY 45
QY 139 MSNPLGLGLVGLVTLVQSSSTSTSIWVSSSLITVRAAIPITMGANIGTSINTIV 198
DB 46 TSNPFGVLGIGMTALIQSSGVTIVGLVSGALLTRQAIGVGMGANIGTIVTSPIL 105
QY 199 ALMQVDRSEFRAPAGATVHDFNWLVLVLPVEVATHYLEITLQIVESHFKNQED 258
DB 106 G-----ILFHF-----LGLGLFYISIKNGDGLQQAADRLR--FYIDKY 112
QY 259 APDLKLVITKPTKLIQVLDKKVISQIAMNDEKAKNSLVKWKCTFTNKTQINVTVPST 318
DB 113 ALPML-----NIGRIL-----FIGAVCLFFTKRTVN-----FKLGNY 112
QY 319 ANCTSPSLCWTGDIQNTWTKNVTYKENIAKCOHIFVNFHLPDLAVGTILLISLVLCGC 378
DB 134 -----NIGRIL-----FIGVGGIFFPALNL--MSG 155
QY 379 LIMIVKILSVLKGQAVIVKKTINTDPPFPFPAWLTGYLAILVAGMFTIVQSSSVFTSA 438
DB 156 MAPLKDL--QVFQDMIELKNPV-----LGVFVGTGLTLIQSSATIGI 199
QY 439 LTPILGIGVITIERAYPLTGSNIGTITTTAILAALASFGNALRSSLOIALCHFFNISI 497
DB 200 LQNLVAGNLIDQGLPVLFGDNIGTITITAILASLANIAAKR-----VAGAHVAFNITG 255
QY 498 -ILWVPIPT-----RLPIRMKGLGNISAKYRWFVYLIIFP--LIP 540
DB 256 VVCVIFLVPFTVLHWFATNLAPENTIAFAHGTFTNTIVQPFPGALAYFVTKIIP 315

RESULT 12

G97926
conserved hypothetical protein spr0439 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C:Accession: G97926
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21428245; PMID:11544234
A:Accession: G97926
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-543 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK99243.1; PID:gl15458006; GSPDB:GN00174
C:Genetics:
A:Gene: spr0439

Query Match 7.3%; Score 262.5; DB 2; Length 543;
Best Local Similarity 22.7%; Pred. No. 7e-11;
Matches 109; Conservative 52; Mismatches 134; Indels 185; Gaps 14;

QY 79 IKWSEDTKGLICFFQGGIGRLILLGLFYFFVCSLDILSSAFQVGVKAGOFFNSIS 138
DB 3 INWQE-----ILFHF-----LGLGLFYISIKNGDGLQQAADRLR--FYIDKY 45
QY 139 MSNPLGLGLVGLVTLVQSSSTSTSIWVSSSLITVRAAIPITMGANIGTSINTIV 198
DB 46 TSNPFGVLGIGMTALIQSSGVTIVGLVSGALLTRQAIGVGMGANIGTIVTSPIL 105

QY 199 ALMQVDRSEFRAPAGATVHDFNWLVLVLPVEVATHYLEITLQIVESHFKNQED 258
DB 106 G-----ILFHF-----LGLGLFYISIKNGDGLQQAADRLR--FYIDKY 112
QY 259 APDLKLVITKPTKLIQVLDKKVISQIAMNDEKAKNSLVKWKCTFTNKTQINVTVPST 318
DB 113 ALPML-----NIGRIL-----FIGAVCLFFTKRTVN-----FKLGNY 112
QY 319 ANCTSPSLCWTGDIQNTWTKNVTYKENIAKCOHIFVNFHLPDLAVGTILLISLVLCGC 378
DB 134 -----NIGRIL-----FIGVGGIFFPALNL--MSG 155
QY 379 LIMIVKILSVLKGQAVIVKKTINTDPPFPFPAWLTGYLAILVAGMFTIVQSSSVFTSA 438
DB 156 MAPLKDL--QVFQDMIELKNPV-----LGVFVGTGLTLIQSSATIGI 199
QY 439 LTPILGIGVITIERAYPLTGSNIGTITTTAILAALASFGNALRSSLOIALCHFFNISI 498
DB 200 LQNLVAGNLIDQGLPVLFGDNIGTITITAILASLANIAAKR-----VAGAHVAFNITG 255
QY 499 L--LWVPIPT-----RLPIRMKGLGNISAKYRWFVYLIIFP--LIP 540
DB 256 VVCVIFLVPFTVLHWFATNLAPENTIAFAHGTFTNTIVQPFPGALAYFVTKIIP 315

RESULT 13

G83825
hypothetical protein BH1407 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: G83825
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, P.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83825
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-543 <STO>
A:Cross-references: GB:AP001511; GB:BA000004; NID:gl0173727; PIDN:BA05126.1; GSPDB:GN01
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1407

Query Match

6.9%; Score 247.5; DB 2; Length 543;
Best Local Similarity 22.1%; Pred. No. 8e-10;
Matches 104; Conservative 58; Mismatches 115; Indels 193; Gaps 15;

QY 90 ILCOFQIGRLILLGLFYFFVCSLDILSSAFQVGVKAGOFFNSISMSNPLGLVIG 149
DB 9 LFWFQGLG--ILFGLIKY-----MGDGLQVAGERLRDL--DKFTTNELMGVLAG 56
QY 150 VLVTVLQSSSTSTSIWVSSSLITVRAAIPITMGANIGTSINTIVVALMOVGDRSEF 209
DB 57 IVTVLLQSTGTGTLTGLVNAQFMGLKQAIGVGMGANIGTIVTAFIIG-----106
QY 210 RRAFAGATVHDFNWLVLVLPVEVATHYLEITLQIVESHFKNQEDAPDLKLVTKP 269
DB 107 -----IKSEVALPIIANGAALIFFIKN-----129
QY 270 FTKLIQVLDKKVISQIAMNDEKAKNSLVKWKCTFTNKTQINVTVPSTANCTSPSLCWT 329
DB 130 -----KKV-----132
QY 330 DGIQNTWTKNVTYKENIAKCOHIFVNFHLPDLAVGTILLISLVLCGLIMIVKILSV 389
DB 133 -----NNIG--QVIF-----GFGTLFYGLNTN-----152
QY 390 LKGOVATVTKTINTDPPFPALIT-----CYLAILVAGMFTIVQSSSVFTSALTPLI 443
DB 153 --GEGNLPUREL-----QAPADLVMSNENPLVGLIGTITFAVQSSSASTGLGQQY 204
QY 444 GIGVITIERAYPLTGSNIGTITTTAILAALASFGNALRSSLOIALCHFFNISG--ILLW 501

Db 205 DQGMDFALPVLFGNIGTITAVLAAGASVAARA-----ALTHVFNLIGTIIVLI 260
QY 502 YFIPETR-----LPIRMAGLGNIS--AKYRWFAPVYLLI 534
Db 261 IIIPTHTIAXLAUVFALNRPMTIAPAGIFNVNTIIQPFPGIILAIIV 310

RESULT 14
E90554
conserved hypothetical protein MYPU_3410 [imported] - Mycoplasma pulmonis (strain UAB CT)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
A;Accession: E90554
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: E90554
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-569 <KUR>
A;Cross-references: GB:AL445566; PID:g14089755; PIDN:CAC13514.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU 3410
A;Genetic code: SGC3

Query Match 6.7%; Score 242.5; DB 2; Length 569;
Best Local Similarity 20.7%; Pred. No. 1.9e-09;
Matches 109; Conservative 84; Mismatches 122; Indels 211; Gaps 23;

QY 91 LCFQIGRILILIGFLYFVCSLDILGSAPQLVGGKMGQFPSSNSIMSNPLGLGIV 150
Db 18 LGWEGI--LLVFG-ISVPLMSIKMSTSRNVGSEKFKIL--LSRSPRIIGIAGF 72

QY 151 LTVLVQSSSTSTSVVMSVSSLTVRAAIPIMINGANIGTSITNTIVAMQVGRSEFR 210
Db 73 AFTSMIQSDGAVALLGAILAFAFDLKGATAFVIGANVGATTSIIVALEQ----- 124

QY 211 RAFAGATVHDFNWLVSIVLLPEVATYHLIIQLIVESFHFKNGEDAPDLLKVIYKP 270
Db 125 -----YFKISNYLLM-----CVIGGFIF----- 143

QY 271 TKLIVQDKKVISQIAMNDEKAKNSLVKIWKCTFTNKTQINVTVPSTANCTSPSLCWD 330
Db 144 -----LFFKK----- 148

QY 331 GIQNTWMKNVYKENTAKCOHIFVNFHPLDLAVGTIILLSLVLGCGCLIMIVKILGVL 390
Db 149 --EKWT-----KIG-FLIFS-----GMIFLGLKILGSV 175

QY 391 KGOVATVTKTINTDPPFPA-----WLTGYLAILVAGMTFIVQSSSVTSALTPLI 443
Db 176 K-----VLIQSPVSDFKKPGQDSANNISFFFSI-----ALTALFQSSATIAIYQAIL 227

QY 444 --GIGVITIRAVPLTIGNSIGTTTALAILAGLSPGNALRSSLOIALCHFFPNISGILM 501
Db 228 SGENILSLSGALVLCANIGTTTITAILAFVS-GB--KNSRIAISWLFNSIALIA 284

QY 502 YPI-----PPTRIPIRMAGLGNISAKYRW-----FAVFYLIIFPFIPIPTVFGLS 547
Db 285 NSLVGVAFAFPVRL---IVGENEIAA---WQLSIAHLNFIPLAVVFFFIKQLV---- 334

QY 548 LAGRWLVGVGVFVFIILIVLCRLQRCPR-----VLPKQLQN 588
Db 335 ---W-----LCFVLKKSEDEKTEGMPLPKLVN 360

RESULT 15

H71283
conserved hypothetical integral membrane protein TP0771 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
A;Accession: H71283
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: H71283
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-593 <COL>
A;Cross-references: GB:AE001248; GB:AE000520; NID:g3323074; PIDN:AAC65739.1; PID:g332307
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0771

Query Match 6.1%; Score 218.5; DB 2; Length 593;
Best Local Similarity 20.7%; Pred. No. 9.9e-08;
Matches 111; Conservative 78; Mismatches 149; Indels 199; Gaps 20;

QY 31 KSKETNNNT---EAPVTKIELLPSYSTATLIDPTEVDVDPNWLPTLODSGINKSERDTK 87
Db 9 KERLTNKHSTVRSVPLRTIDTYPLFL-----W-----WAPMLV 44

QY 88 GKILCFQIGRILILIGFLYFVCSLDILGSAPQLVGGKMGQFPSSNSIMSNPLGLV 147
Db 45 AVLL-----QGIGS-----LGFMLP---GKMLSDGQKGTGSLHKIL--QWMTSCFFAVL 92

QY 148 TGVLVTVLVQSSSTSTSVVMSVSSLTVRAAIPIMINGANIGTSITNTIVAMQVGRS 207
Db 93 TGMATVAVQSSGATVTMTISFINAGVLSLTSQSIGVLGANIGTIVTAMIVALV----- 146

QY 208 EERRAFAGATVHDFNWLVSIVLLPEVATYHLIIQLIVESFHFKNGEDAPDLLKVI 267
Db 147 -----GFOFK----- 151

QY 268 KPFTKLIVQDKKVISQIAMNDEKAKNSLVKIWKCTFTNKTQINVTVPSTANCTSPSLC 327
Db 152 -----LASTAVPAP----- 160

QY 328 WTDGIQNTWMKNVYKENTAKCOHIFVNFHPLDLAVGTIILLSLVLGCGCLIMIVKILG 387
Db 161 ---GIGYF---LTFPKHLHK-----GHLGESIMGFGLFTGL---GLSSSLPPLS 202

QY 388 ----SVLKGQVATVTKTINTDPPFPAWLTGYLAILVAGMTFIVQSSSVTSALTPLI 443
Db 203 VEELSFLKIAVED-----RALSVFVGLSGFVLTVILHSSATTAIVLTMA 248

QY 444 GIGVITIRAVPLTIGNSIGTTTALAILAGLSPGNALRSSLOIALCHFFPNISG----IL 499
Db 249 FGVIGIVEFAASVLSNVSIGSTIDAAIAIGSKLNARRA-----AAHVLFNVFGALVFLM 304

QY 500 LMYPIPTFRLPIRMAG--GLGNISAKYRW--FAVFYLIIFPFIPIPTVFGLSAGRW 553
Db 305 FPHPV-LALLCVLTTPKNSGFDNITVRLALFHSMENIVNTIIVFPFTKHLAAVFEWLI 360

Search completed: August 26, 2003, 15:53:41
Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2003, 15:41:38 ; Search time 26 seconds
(without alignments)
1246.208 Million cell updates/sec

Title: US-10-052-664-1

Perfect score: 3597

Sequence: 1 MAPWPELGDAQPNPKYLEG.....SREAQCEVPASDSKTECTAL 689

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127963 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127963

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1721	47.8	637	1 NPT2 RAT	Q06496 rattus norv
2	1717	47.7	639	1 NPT2 SHEEP	Q97704 oviss aries
3	1698.5	47.2	639	1 NPT2 HUMAN	Q06495 homo sapien
4	1681.5	46.7	642	1 NPT2 RABIT	Q28620 o renal sod
5	1667	46.3	637	1 NPT2 MOUSE	Q08025 mus musculu
6	203	5.6	310	1 Q0EW BACSU	P54463 bacillus su
7	165	4.6	543	1 XJBB ECOLI	P32683 escherichia
8	144.5	4.0	543	1 XJBB SALT	P40730 salmonella
9	139.5	3.9	630	1 YD13 SCHPO	Q92341 schizosacch
10	129	3.6	654	1 PSTA MYCGE	P47651 mycoplasma
11	128.5	3.6	556	1 OCN3 HUMAN	Q75751 homo sapien
12	128	3.6	512	1 COX1 LOCMI	Q36421 locusta mig
13	127.5	3.5	524	1 LCTP BACHD	Q9K529 bacillus ba
14	127	3.5	551	1 OCN3 MOUSE	Q9K529 mus musculu
15	125	3.5	547	1 SNG1 YEAST	P46950 saccharomyc
16	123.5	3.4	551	1 OCN3 RAT	Q88446 rattus norv
17	121.5	3.4	896	1 BOSS DROME	P22815 drosophila
18	121	3.4	508	1 COX1 BLAGE	Q36724 blattella g
19	118	3.3	464	1 NORM PASMU	Q9cmz9 pasteurella
20	116	3.2	448	1 NMTH LISMO	Q8y773 listeria mo
21	116	3.2	1021	1 S123 HUMAN	P55017 homo sapien
22	115	3.2	651	1 PSTA MYCPN	P75185 mycoplasma
23	115	3.2	512	1 COX1 RHISA	Q99818 rhinipcephal
24	114	3.2	517	1 COX1 MYXGL	Q21079 myxine glut
25	114	3.2	893	1 BOSS DROVI	Q24738 drosophila
26	113	3.1	448	1 NMTH LISIN	Q92bt1 listeria in
27	112.5	3.1	518	1 COX1 SQAC	Q9Z252 squalus aca
28	111.5	3.1	517	1 COX1 SCTCA	Q99403 scyllorhinu
29	110.5	3.1	613	1 NUSM POLOR	Q95918 polypetetus
30	110	3.1	429	1 URAA ECOLI	P33780 escherichia
31	110	3.1	475	1 SECY MYCGE	P47416 mycoplasma
32	110	3.1	514	1 COX1 ANOGA	P34838 anopheles g
33	110	3.1	812	1 MPD EUCAI	P57381 buchiera ap

34	110	3.1	1132	1 NUT1 YEAST	P53114 saccharomyc
35	109.5	3.0	388	1 YUBA BACSU	Q32086 bacillus su
36	109	3.0	514	1 COX1 ANOQU	P33504 anopheles g
37	109	3.0	543	1 HTI TRIVI	Q27115 trypanosoma
38	109	3.0	607	1 NUSM MOUSE	P03921 mus musculu
39	108.5	3.0	369	1 Y316 MYCPN	Q50361 mycoplasma
40	108.5	3.0	656	1 SL54 MOUSE	Q9et37 mus musculu
41	108	3.0	356	1 CKF8 MACMU	Q97665 macaca mula
42	107.5	3.0	687	1 AFUB ACTPL	Q44123 actinobacil
43	107.5	3.0	799	1 S6A5 RAT	P58295 rattus norv
44	107.5	3.0	1476	1 CFTR MOUSE	P26361 mus musculu
45	106.5	3.0	197	1 CSP XENLA	O42196 xenopus lae

ALIGNMENTS

RESULT 1					
NPT2 RAT	ID	NPT2 RAT	STANDARD;	PRT;	637 AA.
AC	Q06456;				
DT	01-FEB-1995 (Rel. 31, Created)				
DT	01-FEB-1995 (Rel. 31, last sequence update)				
DT	15-SEP-2003 (Rel. 42, last annotation update)				
DE	Renal sodium-dependent phosphate transporter protein 2 (Sodium/phosphate cotransporter 2) (Na(+)/Pi cotransporter 2) (Renal sodium-phosphate transport protein 2) (Renal Na(+)-dependent phosphate cotransporter 2).				
GN	SLC34A1 OR SLC17A2.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RX	MEDLINE=93317607; PubMed=8327470;				
RA	Magagnin S., Werner A., Markovich D., Sorribas V., Stange G., Biber J., Murer H.;				
RA	"Expression cloning of human and rat renal cortex Na/Pi cotransport.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 90:5979-5983(1993).				
RN	[2]				
RP	DISULFIDE BONDS, AND REVISED TOPOLOGY.				
RX	MEDLINE=20385426; PubMed=10926678;				
RA	Lambert G., Forster I.C., Biber J., Murer H.;				
RT	"Cysteine residues and the structure of the rat renal proximal tubular type II sodium phosphate cotransporter (rat Napi IIA).";				
RL	J. Membr. Biol. 176:133-141(2000).				
CC	-!- FUNCTION: MAY BE INVOLVED IN ACTIVELY TRANSPORTING PHOSPHATE INTO CELLS VIA NA+ COTRANSPORT IN THE RENAL BRUSH BORDER MEMBRANE.				
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-!- TISSUE SPECIFICITY: Kidney.				
CC	-!- SIMILARITY: Belongs to the sodium/phosphate cotransporter family.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
DR	EMBL; L13257; AAC37608.1; -				
DR	PIR; A48189; A48189.				
DR	InterPro; IPR003841; Na/Pi_cotransp.				
DR	Fram; PF02690; Na_Pi_cotrans; 2.				
DR	TIGRFAM; TIGR01013; 2a58; 1.				
KW	Transport; Symport; Sodium transport; Transmembrane; Glycoprotein; Phosphorylation.				
FT	DOMAIN 1 103 CYTOPLASMIC (POTENTIAL).				
FT	TRANSMEM 104 125 ML (POTENTIAL).				
FT	DOMAIN 126 145 EXTRACELLULAR (POTENTIAL).				

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FT TRANSNEM 146 163 M2 (POTENTIAL)..
FT DOMAIN 164 216 CYTOPLASMIC (POTENTIAL)..
FT TRANSNEM 217 236 M3 (POTENTIAL)..
FT DOMAIN 237 345 EXTRACELLULAR (POTENTIAL)..
FT TRANSNEM 346 368 M4 (POTENTIAL)..
FT DOMAIN 369 410 CYTOPLASMIC (POTENTIAL)..
FT TRANSNEM 411 434 M5 (POTENTIAL)..
FT DOMAIN 435 464 EXTRACELLULAR (POTENTIAL)..
FT TRANSNEM 465 485 M6 (POTENTIAL)..
FT DOMAIN 486 511 CYTOPLASMIC (POTENTIAL)..
FT TRANSNEM 512 532 M7 (POTENTIAL)..
FT DOMAIN 533 537 EXTRACELLULAR (POTENTIAL)..
FT TRANSNEM 538 559 M8 (POTENTIAL)..
FT DOMAIN 560 637 LEUCINE-ZIPPER..
FT TRANSNEM 637 677 PHOSPHORYLATION (BY PKC) (POTENTIAL)..
FT MOD RES 506 506 POTENTIAL..
FT DISULFID 225 520
FT DISULFID 306 334
FT CARBOHYD 298 298 N-LINKED (GLCNAC.. ) (POTENTIAL)..
FT CARBOHYD 328 328 N-LINKED (GLCNAC.. ) (POTENTIAL)..
SQ SEQUENCE 637 AA; 68706 MW; 34D02E7817683F42 CRC64;

Query Match 47.8%; Score 1721; DB 1; Length 637;
Best Local Similarity 59.9%; Pred. No. 1e-109;
Matches 348; Conservative 79; Mismatches 120; Indels 34; Gaps 4;

QY 43 PVTKIELPSYATLID-----EPTVEDDPMWLPPTLQDSIKWSDRTKGKILCFQG 96
DB 42 PGTITATSLSPVATLTHSPYGEVLECHDPLPKLAQEEQEPERLSQ-KLAQVTK 100
QY 97 IGRLLILLGLFYFVCSLDILSSAFQVGGKAGOFFNSIMSNPLGLHGVILVTLV 156
DB 101 LLKVLPMGLFYLFCVSLDVLSSAFQAGGVAGDFKDNAILSNPVAGLVGILVTLV 160
QY 157 QSSSTSTSIWVSWSSLLTTRAAPIPIINGANIGTSITNTIVALMQVDSRFRPAGA 216
DB 161 QSSSTSTSIWVSWSSLLTTRAAPIPIINGANIGTSITNTIVALMQVDSRFRPAGA 220
QY 217 TVHDFNLSVLVLLPVEVATHYLEITLTVESPEKNGEDAPDLKVKITKPKLIVO 276
DB 221 TVHDFNLSVLVLLPVEVATHYLEITLTVESPEKNGEDAPDLKVKITKPKLIVO 280
QY 277 LDKKVISQIANDKAKNSLVKTKWCKTFTNKTQINVT----VPSTANCTSPSLCWTG 332
DB 281 LDKSVITSIAVGBSRLNHSIRIWCQPEKTEASTSMRVEAIGSLANTT----- 330
QY 333 QNWTNKNVYKENIAKCOHIWNEHLPDIAVGTILLILSLVLCGLIMVILGSLVKG 392
DB 331 -----NEKCNHIFVDTGLPDLAVGILLGLSLVLCGLIMVILGSLVKG 377
QY 393 QVATVTKTINTDFFPPFAMLTGYLALVAGMTFTVQSSSVFTSALTPLIGIGVITIER 452
DB 378 QVANVIOKVINTDFFAPFTWTVGYFAMVVGASMTFVQSSSVFTSALTPLIGLVISIER 437
QY 453 AYPITLGSNIGTITTAIALAASPGNALRSSLOIALCHFFPNISGILLWPIPTPLR 512
DB 438 AYPITLGSNIGTITTAIALAASPREKISSFOIALCHFFPNISGILLWPIPTPLR 497
QY 513 MAKGLGNISAKYWPVAVFVLLIFPLPLTVFGLSLAGWRVLGVGVVFFVFIILVCLR 572
DB 498 MAKALGRKAKYKFAVFLVLLVFCVLLPLSLVFLVGLSWAGQANVGTPFGALLAFVLVN 557
QY 573 LLQSRCPRLPKKLQNNPFLPWRSLKPDWAVVSKTQCF 613
DB 558 VLQSRSPHLPKWLQWDFLPRMHSLOPLDGLITRATLCY 598

```

RESULT 2

ID NPT2 SHEEP STANDARD; PRT; 639 AA.
 AC Q97704;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

```

15-SEP-2003 (Rel. 42, Last annotation update)
Renal sodium-dependent phosphate transport protein 2 (Sodium/phosphate
cotransporter 2) (Na(+)/Pi cotransporter 2) (Renal sodium-phosphate
transport protein 2) (Renal Na(+)-dependent phosphate cotransporter
2).
DB SLC34A1 OR SLC17A2 OR NPT2.
OS Ovis aries (Sheep).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney cortex;
RA Wood I.S., Ford L.T., Penny J.I., Shirazi-Beechey S.P.;
RT "Characterisation of a Na+-dependent phosphate cotransporter from
ovine renal outer cortex.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY BE INVOLVED IN ACTIVELY TRANSPORTING PHOSPHATE
INTO CELLS VIA NA+ COTransPORT IN THE RENAL BRUSH BORDER
MEMBRANE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the sodium/phosphate cotransporter family.
-----
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBL: AJ001385; CAA04715.1; -.
InterPro: IPR003841; Na/Pi cotranspt.
Pfam: PF02690; Na_Pi_cotrans; 2.
TIGRfam: TIGR01013; za58; 1.
Transfam; Symport; Sodium transport; Transmembrane; Glycoprotein;
Phosphorylation.
KW DOMAIN 1 103 CYTOPLASMIC (POTENTIAL)..
FT TRANSNEM 104 125 M1 (POTENTIAL)..
FT DOMAIN 126 145 EXTRACELLULAR (POTENTIAL)..
FT TRANSNEM 146 163 M2 (POTENTIAL)..
FT DOMAIN 164 185 CYTOPLASMIC (POTENTIAL)..
FT TRANSNEM 186 185 M3 (POTENTIAL)..
FT DOMAIN 186 347 EXTRACELLULAR (POTENTIAL)..
FT TRANSNEM 348 370 M4 (POTENTIAL)..
FT DOMAIN 371 412 CYTOPLASMIC (POTENTIAL)..
FT TRANSNEM 413 436 M5 (POTENTIAL)..
FT DOMAIN 437 466 EXTRACELLULAR (POTENTIAL)..
FT TRANSNEM 467 487 M6 (POTENTIAL)..
FT DOMAIN 488 513 CYTOPLASMIC (POTENTIAL)..
FT TRANSNEM 514 534 M7 (POTENTIAL)..
FT DOMAIN 535 539 EXTRACELLULAR (POTENTIAL)..
FT TRANSNEM 540 561 M8 (POTENTIAL)..
FT DOMAIN 562 639 CYTOPLASMIC (POTENTIAL)..
FT DOMAIN 348 369 LEUCINE-ZIPPER..
FT MOD RES 508 508 PHOSPHORYLATION (BY PKC) (POTENTIAL)..
FT CARBOHYD 298 298 N-LINKED (GLCNAC.. ) (POTENTIAL)..
FT CARBOHYD 323 323 N-LINKED (GLCNAC.. ) (POTENTIAL)..
FT CARBOHYD 330 330 N-LINKED (GLCNAC.. ) (POTENTIAL)..
SQ SEQUENCE 639 AA; 69022 MW; 713E39C54EC3A1F CRC64;

Query Match 47.7%; Score 1717; DB 1; Length 639;
Best Local Similarity 64.9%; Pred. No. 1.9e-109;
Matches 338; Conservative 66; Mismatches 93; Indels 24; Gaps 4;

QY 102 LLIAGFLYFVCSLDILSSAFQVGGKAGOFFNSIMSNPLGLHGVILVTLVQSST 161
DB 106 EMLSFYLFVCSLDVLSSAFQAGGVAGDFKDNAILSNPVAGLVGILVTLVQSST 165
QY 162 STSIWVSWSSLLTTRAAPIPIINGANIGTSITNTIVALMQVDSRFRPAGATVDF 221
DB 166 STSIWVSWSSLLTTRAAPIPIINGANIGTSITNTIVALMQVDSRFRPAGATVDF 225

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QY 222 FNLVSLVLLPVEVATHYLEITOLIVSEFHKNGEDAPDLKVIKPTKLIIVOLDKV 281
 DB 226 FNLVSLVLLPVEVATHYLEITOLIVSEFHKNGEDAPDLKVIKPTKLIIVOLDKV 285
 QY 282 ISOIANDDEKANKSVIKWCKTFTNKTQINVTVPSTANTCSLSLWTDGIONWTKNVT 341
 DB 286 ITSLSAGDESRLNHLRVWC--YNPTEVPTMPRAEANTSM-----RNAT 332
 QY 342 YKENTAKOHLFVNFHLPDLAVGTILLILSLVLCGLIMVLKSLGKGVAVIKKT 401
 DB 333 ----LEKCNHIFVDTGLPDLAVGLILLAGSLALCTCLILVXNLSLKGQVAKVIOKV 388
 QY 402 INTDPPFFAMLTGYLAILYAGMTFIVQSSVFTSALTPLIGIVITIERAYPLTIGSN 461
 DB 389 INTDPPFTWATGYFAMVGVASMTFVQSSVFTSALTPLIGIVISIERAYPLTIGSN 448
 QY 462 IGTITTAIALAGNALRSSLOIALCHFFNFISGILLWYPIPTFRLPIRMAGLGNIS 521
 DB 449 IGTITTAIALAGPREKLSSAFQIALCHFFNFISGILLWYPIPTFRLPIRMAGLGNIS 508
 QY 522 AKYRFVAVYLLIIEFFILPTLVGLSLAGRVLCVGVVFFIILVLCRLQSRCPV 581
 DB 509 AKYRFVAVYLLIIEFFILPTLVGLSLAGRVLCVGVVFFIILVLCRLQSRCPV 568
 QY 582 LPKCLQNNFLELMRSIKPDWAVSKFTGCFQKRCOCOC 622
 DB 569 LPKCLQNNFLELMRSIKPDWAVSKFTGCFQKRCOCOC 602
 RESULT 3
 NPT2 HUMAN STANDARD; PRT; 639 AA.
 ID NPT2 HUMAN STANDARD; PRT; 639 AA.
 AC Q06495;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Renal sodium-dependent phosphate transporter protein 2 (Sodium/phosphate cotransporter 2) (Na+/Pi cotransporter 2) (Renal sodium-phosphate transport protein 2) (Renal Na(+)-dependent phosphate cotransporter 2).
 GN SL34A1 OR SL317A2 OR NPT2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 EN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93317607; PubMed=8327470;
 RA Magagnoli S., Werner A., Markovich D., Sorribas V., Stange G., Biber J., Murer H.;
 RA "Expression cloning of human and rat renal cortex Na/Pi cotransport."; Proc. Natl. Acad. Sci. U.S.A. 90:5979-5983 (1993).
 RL CC -1- FUNCTION: MAY BE INVOLVED IN ACTIVELY TRANSPORTING PHOSPHATE INTO CELLS VIA NA+ COTRANSPORT IN THE RENAL BRUSH BORDER MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: KIDNEY, AND LUNG.
 CC -1- SIMILARITY: Belongs to the sodium/phosphate cotransporter family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL: L13258; AAA36354.1; --
 DR PIR: B48189; B48189.
 DR Genew: HGNC:11019; SLC34A1.
 DR MIM: 182309; --

DR GO: 0005887; C: integral to plasma membrane; TAS.
 DR GO: 0015321; P: sodium-dependent phosphate transporter activity; TAS.
 DR GO: 0007589; P: fluid secretion; TAS.
 DR GO: 0006796; P: phosphate metabolism; TAS.
 DR GO: 0006817; P: phosphate transport; TAS.
 DR InterPro: IPR003841; Na/Pi cotransp.
 DR Pfam: PF02690; Na/Pi cotransp. 2.
 DR TIGRFAMs: TIGR01013; 2a58; 1.
 KW Transport; Symport; Sodium transport; Transmembrane; Glycoprotein; Phosphorylation.
 KW DOMAIN 1 103 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 104 125 M1 (POTENTIAL).
 FT DOMAIN 126 145 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 146 163 M2 (POTENTIAL).
 FT DOMAIN 164 165 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 166 185 M3 (POTENTIAL).
 FT DOMAIN 186 347 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 348 370 M4 (POTENTIAL).
 FT DOMAIN 371 412 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 413 436 M5 (POTENTIAL).
 FT DOMAIN 437 466 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 467 487 M6 (POTENTIAL).
 FT DOMAIN 488 513 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 514 534 M7 (POTENTIAL).
 FT DOMAIN 535 539 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 540 561 M8 (POTENTIAL).
 FT DOMAIN 562 639 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 639 669 LEUCINE-ZIPPER.
 FT MOD_RES 508 508 PHOSPHORYLATION (BY PKC) (POTENTIAL).
 FT CARBOHYD 298 298 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 323 323 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 639 AA; 68937 MW; 65D21D968C35D61B CRC64;
 Query Match 47.2%; Score 1698.5; DB 1; Length 639;
 Best Local Similarity 58.7%; Pred. No. 3.4e-108;
 Matches 348; Conservative 82; Mismatches 118; Indels 45; Gaps 9;
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 DB 42 PGTSAFAPSLGVALAHTCPCGVLRHEP--LPKALAE-----EQPSRLVPK 93
 QY 94 FOGIGRLI-----LLGLFYFFVCSLDLSSAFQVGGKAGVFPFSSNMSNPLGLVIG 149
 DB 94 LEQAGAMLLKVLPLMLTLYLFCVSLDMLSSAFQAGKAGVDFKDALNSNPAVLGVG 153
 QY 150 VLVTVLVQSSSTSTSIIVSWSSLLTVRAIPINGANIGTSITNTIIVLMQVDSSEF 209
 DB 154 ILVTVLVQSSSTSTSIIVSWSSGLLVSSAIPITMSNIGTSITNTIIVLMQVDSSEF 213
 QY 210 RRAFAGATVDFNWLVLVLPVAVATHYLEITOLIVSEFHKNGEDAPDLKVIKPT 269
 DB 214 RRAFAGATVDFNWLVLVLPVAVATHYLEITOLIVSEFHKNGEDAPDLKVIKPT 273
 QY 270 FTKLIVOLDKKVISQIANDDEKANKSVIKWCKTFTNKTQINVTVPSTANTCSLSLW 329
 DB 274 FTKLIVOLDKKVISQIANDDEKANKSVIKWCKTFTNKTQINVTVPSTANTCSLSLW 320
 QY 330 DGIQNWTKNVTYKEMIAKCOHIFVNFHLPDLAVGTILLILSLVLCGLIMVLKSLG 389
 DB 321 EANGSQTIGNAT-----MEKCNHIFVDTGLPDLAVGLILLAGSLALCTCLILV 376
 QY 390 LKGQVATVTKTINTDPPFFAMLTGYLAILYAGMTFIVQSSVFTSALTPLIGIVIT 449
 DB 377 LKGQVATVTKTINTDPPFFAMLTGYLAILYAGMTFIVQSSVFTSALTPLIGIVIS 436
 QY 450 TERAYPLTIGSNIGTITTAIALAGPREKLSSAFQIALCHFFNFISGILLWYPIPT 509
 DB 437 TERAYPLTIGSNIGTITTAIALAGPREKLSSAFQIALCHFFNFISGILLWYPIPT 496
 QY 510 PIRMAKGLGNISAKYRFVAVYLLIIEFFILPTLVGLSLAGRVLCVGVVFFIILV 569
 DB 497 PIRMAKGLGNISAKYRFVAVYLLIIEFFILPTLVGLSLAGRVLCVGVVFFIILV 556

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QY 570 CLLELOSCEPRVLPKLLQNNWELPLMWSLKWDVAVSKFTGCFQMRCCCCCR 622
SQ SEQUENCE 642 AA; 69431 MW; A4985C001642A8B CEC64;
Query Match 46.7%; Score 1681.5; DB 1; Length 642;
Best local similarity 58.6%; Pred. No. 4.9e-107;
Matches 349; Conservative 77; Mismatches 119; Indels 51; Gaps 10;

QY 43 PVTKEILPSSYSTATLID-----RPTVEDDPWMLPT-----LQDSGIKWS--RDT 86
Db 45 PGTSAFAPSLSPVALTERGCPYGARERHEP--LPKALAEEOQPESG--WAQELRPT 100
QY 87 KKKILCFQGGIGRLLILGLFYFVCSLDILSSAFOLVGGKAGOFFSNSSIMSNPLGL 146
Db 101 AMTLL-----KLPLMVTFLYFVCSLDILSSAFOLVGGKAGOFFSNSSIMSNPLGL 153
QY 147 VIGVLTAVTVVQSSSTSTSIIVSVSSSLLTYRAIRPIIMGANIGTSITITVIALMOVQDR 206
Db 154 VVGILVTVLVQSSSTSTSIIVSVSSSLLTYRAIRPIIMGANIGTSITITVIALMOVQDR 213
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Db 214 TDFRRAFAGATVDFEFNLSVLVLPVEVATHYLEITOLIVSFHFKNGEDAPLLKVI 273
QY 267 TKPFTKLIQVOLDKKVISQIAMNDEKAKNSLVKWKCTFNKTQINVTVPSTANCTSPSL 326
Db 274 TEPFTKLIQVOLDKKVISQIAMNDEKAKNSLVKWKCTFNKTQINVTVPSTANCTSPSL 327
QY 327 CWTGDIQNTWTKNTYKENIAKOHFVNFLPDLAVGTITLLILSLVCGCLIMVKIL 386
Db 328 SRTHG--NATME-----KCNHIFVDVTDPLAVGLILLAGSVLLCTCHILVKKML 376
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Db 497 TRLPRMAGKGNISAKYRFAVYVLIFFFLIPLTVGLSLAGWLVGVGVVVFII 556
QY 567 LVLCRLQLQSCPRVLPKLLQNNWELPLMWSLKWDVAVSKFTGCFQMRCCCCCR 622
Db 557 FVVLINVLQSSRSPGLPKWLTQWDFLPHMWSLQPLDLHLTHAT-----LCCSR 605

RESULT 5
NPT2_MOUSE STANDARD; PRT; 637 AA.
ID NPT2_MOUSE 642 AA; 69431 MW; A4985C001642A8B CEC64;
AC Q62564; Q62110; Q62111; Q62112; Q62113; Q62114; Q62115; Q62116;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Renal sodium-dependent phosphate transporter protein 2 (Sodium/phosphate
DE cotransporter 2) (Na+/Pi cotransporter 2) (Renal sodium-phosphate
DE transport protein 2) (Renal Na(+)-dependent phosphate cotransporter 2)
DE (Napi-7).
DE SLC34A1 OR SLC17A2 OR NPT2.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STEIN-BALE/c; TISSUE=Kidney cortex;
RX MEDLINE=96006598; PubMed=7478940;
RA Hartmann C.M., Wagner C.A., Busch A.E., Markovich D., Biber J.,
RA Laag F., Murer H.;
RT "Transport characteristics of a murine renal Na/Pi-cotransporter.";
RL Pfugers Arch. 430:830-836 (1995).
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RESULT 4

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NPT2_MOUSE STANDARD; PRT; 642 AA.
ID NPT2_MOUSE 642 AA; 69431 MW; A4985C001642A8B CEC64;
AC Q28620; Q28621; Q28622; Q28623; Q28624; Q28625; Q28626; Q28627; Q28628; Q28629; Q28630; Q28631; Q28632; Q28633; Q28634; Q28635; Q28636; Q28637; Q28638; Q28639; Q28640; Q28641; Q28642; Q28643; Q28644; Q28645; Q28646; Q28647; Q28648; Q28649; Q28650; Q28651; Q28652; Q28653; Q28654; Q28655; Q28656; Q28657; Q28658; Q28659; Q28660; Q28661; Q28662; Q28663; Q28664; Q28665; Q28666; Q28667; Q28668; Q28669; Q28670; Q28671; Q28672; Q28673; Q28674; Q28675; Q28676; Q28677; Q28678; Q28679; Q28680; Q28681; Q28682; Q28683; Q28684; Q28685; Q28686; Q28687; Q28688; Q28689; Q28690; Q28691; Q28692; Q28693; Q28694; Q28695; Q28696; Q28697; Q28698; Q28699; Q28700; Q28701; Q28702; Q28703; Q28704; Q28705; Q28706; Q28707; Q28708; Q28709; Q28710; Q28711; Q28712; Q28713; Q28714; Q28715; Q28716; Q28717; Q28718; Q28719; Q28720; Q28721; Q28722; Q28723; Q28724; Q28725; Q28726; Q28727; Q28728; Q28729; Q28730; Q28731; Q28732; Q28733; Q28734; Q28735; Q28736; Q28737; Q28738; Q28739; Q28740; Q28741; Q28742; Q28743; Q28744; 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CC -----
DR ENBL; U00006; AAC43114.1; -.
DR ENBL; AE000475; AAC76990.1; -.
DR ENBL; AE015417; AAN45511.1; -.
DR PIR; C65209; C65209.
DR EcoGene; EG11919; yjbb.
DR InterPro; IPR003841; Na/Pi cotranspt.
DR InterPro; IPR004633; Napi cotransptII.
DR Pfam; PF02690; Na_Pi_cotrans; 1.
DR TIGRFAMs; TIGR01013; 2a58; 1.
DR TIGRFAMs; TIGR00704; Napi cotrn rel; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 48 68 POTENTIAL.
FT TRANSMEM 76 96 POTENTIAL.
FT TRANSMEM 99 119 POTENTIAL.
FT TRANSMEM 134 154 POTENTIAL.
FT TRANSMEM 175 195 POTENTIAL.
FT TRANSMEM 196 216 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 274 294 POTENTIAL.
SQ SEQUENCE 543 AA; 59466 MW; BA97149CC41A093F CRC64;

Query Match 4.6%; Score 165; DB 1; Length 543;
Best Local Similarity 20.6%; Pred. No. 0.00058;
Matches 94; Conservative 58; Mismatches 134; Indels 170; Gaps 14;

Qy 100 LILLIGLYFFVCSLDLSAFLQVGGKAGQFSSNSINPLGLVIGLVTVLQSS 159
Db 4 LHLLSAVALLVWGTHTVGTGMVFGARLTVLSR-SVEKLP-LAFCAGIGTALVQSS 61
Qy 160 STSTSVVMSVSSLLTVRAAIPIMGANIGTSTNTIVTALMVQVDRSEFRAPAGATVH 219
Db 62 NATTLVTSFVAQDLVALPALVILGADVGTALMARILTF----- 102
Qy 220 DFFNWLVLVLLPVEVATHYLEITQLIVESFHFKNGEDAPDLLKVTIKFPLVQDK 279
Db 103 -DLSWLSPLLI-----FIGVIFPLGR 122
Qy 280 KVISQIANDEKAKVSLVWCKTFTNKTQINTVTPSTANCYSPSLCWTGIONWTMKN 339
Db 123 K-----QSRAGQLGRV----- 133
Qy 340 VTYKENIAKCHIFVNFPLDLAGVTLLILLLLVLCGLIMIVKILGSLVKGQVATVIK 399
Db 134 -----GIGLILLALEL-----IVQAVTPTQANGVQVI- 163
Qy 400 KTINTDPPFPFAMLTG--YLAILVAGMTFTVQSSVFTSALTPLIGIGVITIERAYPLT 457
Db 164 -----FASLTGILLDALIGAMPALISYSSLAVALLTATLTAAGIISFPVALCLV 213
Qy 458 LGSNIGTTTTAILAALASPCNALRSLOIALCHFFFNISGILLWYPIPTPLIPMAKGL 517
Db 214 IGANIGSGELLAMNNSAANAAR-----VALGSLFLKVLGSLI--ILPFVHL---LAFMT 264
Qy 518 GNISAKYR-----WFAFVY-----LIIFPLIPLTVF 544
Db 265 GKLSLPKALVYIYFVFNVLVRLVLMPLFVDPMARF 300

RESULT 8
YJBB SALTY
ID YJBB SALTY STANDARD; PKT; 543 AA.
AC P40730;
DT 01-FEB-1995 (Rel. 31, Created)

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DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yjbb.
GN YJBB OR STM4189;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE OF 492-543 FROM N.A.
RC STRAIN=LT2; PubMed=8282693;
RX Conlin C.A., Hakensson K., Liljas A., Miller C.G.;
RA "Cloning and nucleotide sequence of the cyclic AMP receptor protein-
RT regulated Salmonella typhimurium pepB gene and crystallization of its
RT product, an alpha-aspartyl dipeptidase."
RL J. Bacteriol. 176:1166-172(1994).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: TO B.SUBTILIS YQEW.
CC -----
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CC -----
DR ENBL; AE008896; AAL23013.1; -.
DR ENBL; U01246; -. NOT ANNOTATED_CDS.
DR StyGene; SGI0492; yjbb.
DR InterPro; IPR003841; Na/Pi cotranspt.
DR InterPro; IPR004633; Napi cotransptII.
DR Pfam; PF02690; Na_Pi_cotrans; 1.
DR TIGRFAMs; TIGR01013; 2a58; 1.
DR TIGRFAMs; TIGR00704; Napi cotrn rel; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 1 21 POTENTIAL.
FT TRANSMEM 76 96 POTENTIAL.
FT TRANSMEM 99 119 POTENTIAL.
FT TRANSMEM 134 154 POTENTIAL.
FT TRANSMEM 175 195 POTENTIAL.
FT TRANSMEM 196 216 POTENTIAL.
FT TRANSMEM 238 258 POTENTIAL.
FT TRANSMEM 274 294 POTENTIAL.
SQ SEQUENCE 543 AA; 59444 MW; 434D9F724DFEB67 CRC64;

Query Match 4.0%; Score 144.5; DB 1; Length 543;
Best Local Similarity 20.2%; Pred. No. 0.014;
Matches 89; Conservative 53; Mismatches 134; Indels 165; Gaps 13;

Qy 100 LILLIGLYFFVCSLDLSAFLQVGGKAGQFSSNSINPLGLVIGLVTVLQSS 159
Db 4 LHLLSAVALLVWGTHTVGTGMVFGARLTVLSR-SVEKLP-LAFCAGIGTALVQSS 61
Qy 160 STSTSVVMSVSSLLTVRAAIPIMGANIGTSTNTIVTALMVQVDRSEFRAPAGATVH 219
Db 62 NATTLVTSFVAQDLVALPALVILGADVGTALMARILTF----- 102
Qy 220 DFFNWLVLVLLPVEVATHYLEITQLIVESFHFKNGEDAPDLLKVTIKFPLVQDK 279

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Qy 538 LIP---LTVFGLSLAGWR 552
 Db 579 LVPAVLSFELAAAFWQ 596

Best Local Similarity 19.3%; Pred. No. 0.2;
 Matches 122; Conservative 97; Mismatches 242; Indels 172; Gaps 26;

Qy 90 ILCPFOGIGELILL-----LGLYFFVCS-----LDLSSAFQVGGMACQOFF 133
 Db 71 LVSVISGALITIASYIGVTSFFLVYRCKPKIRKSLIIDILSGIPSVIFGLFASQIL 130
 Qy 134 SNSSIMSNPLGLVIGLVTVLVVSSSTSTSVVSVSSSLTVAALPIIMGANIGTSI 193
 Db 131 ---SIFPFDILKLPPLSLNVLNIAIPLIPVISLITVNTLVYVNDI---ISVVVSLGENK 186
 Qy 194 TMTVALMOVDRSE-----FRRAPAGATVDFNMLSVLVLPPVEVATHYLEITQ 245
 Db 187 TSAIYKIIKKEIKPOLTVILTAFARAISETMAVNF-----VLQSVNYQEVINN 235
 Qy 246 -----LIVESPEF-KNGEDA-----PDLK 264
 Db 236 NRFTSLDKTSGSVSTFISGNGEQINGVLYIFGIIILVLSLNFPAIWSANPKTLE 295
 Qy 265 VTEPFTKLIQDKKVISQIAMN-----DEKAKKSLVKIWKCTFTKTKQINVTPEST 318
 Db 296 --RYPFLKLSNFIYOVWFIPNIAISALFVDLTSTQSVKLI-----KVN----- 338
 Qy 319 ANCTSPSLWDGION--WTMKQVYKENIAKCHIFVAFHPLDPAVGTILLISLVLVC 376
 Db 339 -NINERSLFFKRLQSVWIKLVFLK-----IFQELICTFLAFGVLAILLFVFIN 389
 Qy 377 GCLTMIVKILGSLV-----KQVATVKKITINTDPPFPA-----MLTGV-LAILV 421
 Db 390 GS--VAIINNNGSTVFSFADSTGRALVNTLVILITITITFPLALLIAILNLYNNKVV 447
 Qy 422 GAGMTFIVQSSSVFTSALTPLIGIVITIERAYPLTIGNIGTITTA-----ILAA 472
 Db 448 KNVFNVFIDLSLSPSIYYGLFGLSFFL--RVQLSAGGANGTSLIAGLITISVILLFL 505
 Qy 473 LASGNALRS-SLQIALCHFFPNIS-----GILLWYPIPTPL-----PI 511
 Db 506 IRTCCQALNNVSDLRISAFALGISKREVIKTVLPSALKGLIVALILISINRIIETAPF 565
 Qy 512 RMAGLGNISAKYRFAVFLIIPFLIPLTVFG--LSLAGWRVLVGVGVFVFIILVL 569
 Db 566 FITLSGSSN-----LFHSLPGQTITRIYQGLFISNSNAISVLTSLSVSVFLIL 618
 Qy 570 CIRLLQRCPRVLPKLQWNPFLNMRSLKPW 602
 Db 619 LIFFSVLIPSLFLNKLQKWLVIKSKFQSKFM 651

RESULT 11

OCN3 HUMAN STANDARD; PRT; 556 AA.
 ID OCN3 HUMAN STANDARD; PRT; 556 AA.
 AC 075751; O9UP02;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Organic cation transporter 3 (Extraneuronal monoamine transporter)
 DE (EMT) (Solute carrier family 22, member 3).
 GN SLC22A3 OR EMT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE=Kidney;
 RX MEDLINE=9921254; PubMed=10196521;
 RA Gruendemann D., Schechinger B., Rappold G.A., Schoemig E.;
 RT "Molecular identification of the corticosterone-sensitive
 extraneuronal catecholamine transporter.";
 RL Nat. Neurosci. 1:349-351 (1998).
 RN [2]
 RP SEQUENCE OF 513-556 FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=99134299; PubMed=9933568;

RESULT 10

PSTA MYCGE STANDARD; PRT; 654 AA.
 AC P47651;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphate transport system permease protein pstA homolog.
 GN PSTA OR MG411.
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RX MEDLINE=96026346; PubMed=7569993;
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Furmann J.L.,
 RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
 RA Tomb J.-F., Dougherty B.A., Bort K.F., Hu P.-C., Lucier T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 RT "The minimal gene complement of Mycoplasma genitalium.";
 RL Science 270:397-403 (1995).
 RN [2]
 RP SEQUENCE OF 136-211 FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RX MEDLINE=94075230; PubMed=8253680;
 RA Peterson S.N., Hu P.-C., Bort K.F., Hutchison C.A. III;
 RT "A survey of the Mycoplasma genitalium genome by using random
 sequencing.";
 RL J. Bacteriol. 175:7918-7930 (1993).
 CC -!- FUNCTION: COULD BE PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM FOR PHOSPHATE; PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION
 CC OF THE SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM PERMEASE FAMILY. CYSTW SUBFAMILY.
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 CC
 CC ENBL; U39723; AAC71639.1; --
 CC ENBL; U01746; AAD10559.1; --
 CC FIR; E64245; E64245.
 CC TIGR; MG411; --
 CC InterPro: IPR000515; BPD transp.
 CC Pfam: PF00528; BPD transp; 2.
 CC PROSITE: PS00402; BPD TRANSP INN MEMBER; FALSE NEG.
 KW Transport; Phosphate transport; Transmembrane; Complete proteome.
 FT TRANSMEM 22 42 POTENTIAL.
 FT TRANSMEM 64 84 POTENTIAL.
 FT TRANSMEM 113 133 POTENTIAL.
 FT TRANSMEM 143 163 POTENTIAL.
 FT TRANSMEM 368 388 POTENTIAL.
 FT TRANSMEM 418 438 POTENTIAL.
 FT TRANSMEM 454 474 POTENTIAL.
 FT TRANSMEM 486 506 POTENTIAL.
 FT TRANSMEM 535 555 POTENTIAL.
 FT TRANSMEM 613 633 POTENTIAL.
 SQ SEQUENCE 654 AA; 73525 MW; 997BD093F7A907B4 CRC64;

Query Match

3.6%; Score 129; DB 1; Length 654;


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CC -----X80245; CRA56527.1; --
DR EMBL; T11467;
DR HSSP; P00396; 20CC.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PRO1165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Oxidoreductase; Heme; Copper; Mitochondrion; Transmembrane;
KW Respiratory chain; Inner membrane.
FT METAL 60 IRON (HEME A AXIAL LIGAND) (PROBABLE).
FT METAL 239 COPPER B (PROBABLE).
FT METAL 243 COPPER B (PROBABLE).
FT METAL 289 COPPER B (PROBABLE).
FT METAL 290 COPPER B (PROBABLE).
FT METAL 375 IRON (HEME A3 AXIAL LIGAND) (PROBABLE).
FT METAL 377 IRON (HEME A3 AXIAL LIGAND) (PROBABLE).
FT METAL 377 IRON (HEME A AXIAL LIGAND) (PROBABLE).
FT CROSSLINK 239 1'-histidyl-3'-tyrosine (by similarity).
SQ SEQUENCE 512 AA; 56814 MW; 98031A229B00511C CRC64;

Query Match 3.6%; Score 128; DB 1; Length 512;
Best Local Similarity 20.1%; Pred. No. 0.18; Indels 274; Gaps 31;
Matches 122; Conservative 61; Mismatches 150;

QY 104 LGFLYFFVCSIDLSSAFOLVGGMAGOFFENSSIMENPLGLVIGLVITVLVQSSTST 163
DB 14 IGTLYEF-----GAWAGVGTSMIIRAEIG-----PGT 45
QY 164 SIIVSMVSSSLTVAAPIT-----INGANIGTSINTVALMQVGRSFRAPAGATVHD 220
DB 46 MINDDOLYVITAHAFVIMFFVMVPIG-GFGNVLVPLMIGAPDAPPR-----MNN 98
QY 221 FFWLSVLVLLPEVATHYLEITOLIVESFHPKNGSDA-----PDLKLVITKPTKL-- 273
DB 99 MSFW-----LLPSLT-----LLMSVVDVNGAGTGTWYPLASVIAHSGASVDL 144
QY 274 -IVOLDKKVISOI--AMDEKANKSLVKIWCKTFTNKTOINTVSTANCTSPSLCWT 330
DB 145 AIFSLEHLAGVSSILGAIN-----FITTAIINRSNNNTLDQT-----PLFVKS- 186
QY 331 GLQNTWKNVYKENTAKCOHIFVPHLPDLAVGTILLISLVLCGLIMIVKILGSVL 390
DB 187 -----VAITALLALLSLPLVLAGAITML----- 208
QY 391 KGQVATVTKTINTDRPEP-----PAWLGTG-----YLAILVAG----- 424
DB 209 -----LTDRLNLTSPFDAGGDPILYQHLNFPPGHPYVILLPGGLIISHIVCOESG 262
QY 425 -----MTFVQSSVFTSALTPLPIGIVTITERAY----- 454
DB 263 KIESFGTIGMTYAMLSTGLMGTIVWAHEWFT-----VGMVDVT--RAYFTSATMIIAVP 314
QY 455 -----PL--TLG-----SNIGTTTAAIALAASPGNALSSLOIA 487
DB 315 TGKIVFWMATLYGTKEKNPPLWALGFIFLFTNGGLGLVIA-----NSSLDIV 365
QY 488 L-----CHPFFNIS-----GILLWYPIPTPLPIRMAGKLGNISAKYRWFVAFY 531
DB 366 LHDYVVVAHSHVYVNGAVFALMGILLQWYPL-FTGLTWN-----KWLKIQF 413
QY 532 LIIPFLPIPLTVFG-----LSIAG-----NRVLVGVGVV-----VFIIILVLC 570
DB 414 TIMFIG-VNLTFFQHPGLAGNPRYSYDPDAVTSNNVSSIGSTISITGIIMFILW 472
QY 571 LKLQSR 577
DB 473 ESMIKOR 479

RESULT 13
LCCTP_BACHD
ID LCCTP_BACHD STANDARD; PRT; 524 AA.
AC Q9K529;
```

```
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-lactate permease.
GN LCCTP OR BH3936.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]_TaxID=86665;
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -!- FUNCTION: May play a role in L-lactate transport.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: BELONGS TO THE LACTATE PERMEASE FAMILY.
CC
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CC
CC EMBL; AF001520; BAB07655.1; -.
DR PIR; H84141; H84141.
DR InterPro; IPR003804; Lactate perm.
DR Pfam; PF02652; Lactate_perm; 1.
DR TIGRFAMs; TIGR00795; LCCTP; 1.
KW Transport; Transmembrane; Complete proteome.
FT TRANSMEM 12 34 POTENTIAL.
FT TRANSMEM 38 60 POTENTIAL.
FT TRANSMEM 67 89 POTENTIAL.
FT TRANSMEM 127 149 POTENTIAL.
FT TRANSMEM 156 178 POTENTIAL.
FT TRANSMEM 193 215 POTENTIAL.
FT TRANSMEM 224 246 POTENTIAL.
FT TRANSMEM 250 267 POTENTIAL.
FT TRANSMEM 297 319 POTENTIAL.
FT TRANSMEM 339 361 POTENTIAL.
FT TRANSMEM 374 396 POTENTIAL.
FT TRANSMEM 411 433 POTENTIAL.
FT TRANSMEM 505 522 POTENTIAL.
SQ SEQUENCE 524 AA; 55628 MW; 0376ED4D9A31AFF6 CRC64;

Query Match 3.5%; Score 127.5; DB 1; Length 524;
Best Local Similarity 18.2%; Pred. No. 0.2;
Matches 83; Conservative 83; Mismatches 138; Indels 153; Gaps 21;

QY 87 KGKILCFQOIGR-----HLLGLGLY-----FFVCSLDILSSAFQ----- 122
DB 102 RGSII-----GISRDQRIQLLIGFCFNAFLGAGRGVPIAICAVLLVSLGFKPLQAML 157
QY 123 -LVGKMGAGOFFPNSIMENPLGLVIGLVITVLVQSSSTSTSIIVSVSSSLITVRAAI 181
DB 158 CLHANGASGAFGA-----IGIPVGIIDTLGLEGQVTSMDVSN-MTALTLPWINFTI 207
QY 182 PLINGANIGTSINTVALMQVGRSFRAPAGATVHDFFNWLVLVLLPEVATHYLE 241
DB 208 PFL-----LIWLMD-----SNWGIKEILFALLIVTSVY 235
QY 242 IITQILVSEFHFNGEDAPDLKLVITKPTKLIVQDKK-----VISQIANNDEKAK 293
DB 236 TVSQALLITIF-----IGPELADIIPSLLTWGLLALFLRWQPRNTFLNNGCSESHAS 289
QY 294 NKSIVKIVCKTFTNKTOINTVSTANCTSPSLCWTGDIGIONWTKNVTYKENTAK----- 348
```

Db 290 LKDVIKAW-----SPFLLTMFVFLWSLP--AFKGLLABGGALE 326
 Qy 349 -COHLEVFHLEPDL-----AVGTLLLSLLVLCGLIMVILKILGSLVKQVATV 397
 Db 327 FAKWAFV---VFGSIEVGVDFTGATGAILLAATVTTTKMKRMK-----ESISL 375
 Qy 398 IKKTINTDPPFPFAM---LAGYLAILVAGMTF---IVQSSSVFTSALTPLIG-IGVI- 448
 Db 376 LKKVI-VDFSIPIMWICAILGIAKMTYGLTWMALGEAVATGAPFPFSLPILGWIGVM 434
 Qy 449 -----TIRAVPLILGNIQTMTTALAMASPG 477
 Db 435 TGSVVNNLTLEPIQTAGAIIGTNPISLVAANTAGG 471
 RESULT 14
 OCN3 MOUSE
 ID OCN3 MOUSE STANDARD; PRT; 551 AA.
 AC Q9WTW5; Q9R209;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Organic cation transporter 3 (Solute carrier family 22, member 3).
 GN SLC22A3 OR OCT3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 EN [1]
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=99134299; PubMed=9933568;
 RA Verhaagh S., Schweifer N., Barlow D.P., Zwart R.;
 RT "Cloning of the mouse and human solute carrier 22a3 (SLC22a3)
 RT identifies a conserved cluster of three organic cation transporters
 RT on mouse chromosome 17 and human 6q26-q27.";
 RL Genomics 55:209-218 (1999).
 RN [2]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE=Kidney;
 RX MEDLINE=20425388; PubMed=10966924;
 RA Wu X., Huang W., Ganapathy M.E., Wang H., Kekuda R., Conway S.J.,
 RA Leibach F.H., Ganapathy V.;
 RT "Structure, function, and regional distribution of the organic cation
 RT transporter OCT3 in the kidney.";
 RL Am. J. Physiol. 279:F449-F458 (2000).
 CC -I- FUNCTION: Mediates potential-dependent transport of a variety of
 CC organic cations. May play a significant role in the disposition of
 CC cationic neurotoxins and neurotransmitters in the brain.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA AND IN KIDNEY
 CC CORTEX BUT NOT MEDULLA. LOW LEVELS FOUND IN BRAIN. IN THE KIDNEY,
 CC EXPRESSED SPECIFICALLY IN THE PROXIMAL AND DISTAL CONVOLUTED
 CC TUBULES AND WITHIN BOWMAN'S CAPSULE BUT NOT IN THE
 CC GLOMERULUS.
 CC -I- DEVELOPMENTAL STAGE: LEVELS ARE HIGH DURING GESTATION BUT DECREASE
 CC GREATLY TOWARDS THE END OF GESTATION.
 CC -I- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. ORGANIC
 CC CATION SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; AF078750; RAD20978.1; -.
 DR EMBL; AF078748; RAD20238.1; -.
 DR EMBL; AF082566; RAD53007.1; -.
 DR MGD; MGI:1333817; SLC22a3.
 DR InterPro; IPR007114; MFS.

DR InterPro; IPR004749; Orgcat transp.
 DR InterPro; IPR005828; Sub transporter.
 DR InterPro; IPR005829; Sug transporter.
 DR InterPro; IPR003663; Sug transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 DR TIGRFAMs; TIGR00898; 2A0119; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; FALSE NEG.
 KW Transport; ion transport; Transmembrane; Glycoprotein.
 FT TRANSMEM 21 POTENTIAL.
 FT TRANSMEM 177 197
 FT TRANSMEM 236 256 POTENTIAL.
 FT TRANSMEM 264 284 POTENTIAL.
 FT TRANSMEM 376 396 POTENTIAL.
 FT TRANSMEM 464 484 POTENTIAL.
 FT TRANSMEM 493 513 POTENTIAL.
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 99 99 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 317 317 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 551 AA; 61052 MW; C4D66AAC2EFCFDB CRC64;
 Query Match 3.5%; Score 127; DB 1; Length 551;
 Best Local Similarity 20.4%; Pred. No. 0.23;
 Matches 112; Conservative 73; Mismatches 205; Indels 160; Gaps 26;
 Qy 49 LIPSYSTAT-LIDEPTEVDPPNLFLODSGIKWSERDTGKILCFQIGRLILLOFL 107
 Db 94 LLEATNTSSELSCDPLTAPNRSAPLVSCSG-DWRYVETHSTIVSQFD----- 140
 Qy 108 YFVCS---LDLSSAFOLVGKMGAGOFFSNSIMSNPLGLV---IGLVTVINQSSS 160
 Db 141 --LUCSNAMLDLTOALNL--GFLGAF-----TLGVAADRYGRLLIYLISCFG 186
 Qy 161 TS-TSIVVSMVSS-SLLTVRAAIPIMGANIGTSITNTVIALMOVGDSEFRFAAGATV 218
 Db 187 VGLTGVVAPAPNFSVFVIFRFLQGVFGK--GAWMTCFVIVTEIVGSK--QRRIVGVI 241
 Qy 219 HDEFNWLVLVLLPVEVAT-HYLEITOLIVESHFP-----KNGEDAP 260
 Db 242 QMFET-LGIILFGLIAYFTFSWQGLAISLPSFLIYYVVPSPRWLITRKQGEKAL 300
 Qy 261 DLKLVITKPTLLVQLDKKVISQIAMNDEKAKNSLVKWKCTFTNKTQINVTVPSTAN 320
 Db 301 QILRAVAKNGKHL-----SSNYSFIVTDEVSNPSCLDL-----VTFQWRK 344
 Qy 321 CTSPLCWTDGIONWTKVYKENIAKQHI FVNPHLPDLAVGTILLILSLVLCGLI 380
 Db 345 CTLILMF-----AWFSAVYQGLVWELIGLGNLYIDPFISGLVLPGLLIL----- 393
 Qy 381 MIVKILGSLVKQVAIVIKKT---INTDPPFPFALVGLIILVGNMGVTFVQSSSVFTS 437
 Db 394 LTERLGRURFFAASNIYAGVSCLVTAFLPEGIPWLTVTATLGRIGITMAFEIVLYNS 453
 Qy 438 ALTPILGIGVITIERAYPLTLGNSIGTITTTTALAALASPCNALRSSLIQALCHFFFNISG 497
 Db 454 EL-----YPTLL-RNFGV-----SLCSGLCDF----- 474
 Qy 498 ILLWYPIPTLPIRWAKGLGNISAKYKWPFAVYLIIFPFILPLTVFGL--SLAGWRVLY 555
 Db 475 -----GGIAP---FLFRLLAAIWLELPLIFIGILASVCGGLVML 511
 Qy 556 -----GVGVP 560
 Db 512 LPETKGIAPL 521
 RESULT 15
 SNG1 YEAST
 ID -SNG1 YEAST STANDARD; PRT; 547 AA.
 AC P46950;
 DR 01-NOV-1995 (Rel. 32, Created)

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OM protein - protein search, using sw model

Run on: August 26, 2003, 15:47:17 ; Search time 118 Seconds
(without alignments)
1506.765 Million cell updates/sec

Title: US-10-052-664-1
Perfect score: 3597
Sequence: 1 MAPPELGDAQPNPKYLEG.....SREAQEVPAQSKTECTAL 689

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_plant:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3594	99.9	689	4 Q9P0V7	Q9P0V7 homo sapien
2	3570.5	99.3	690	4 Q95436	Q95436 homo sapien
3	3023	84.0	591	4 Q8V4A9	Q8V4A9 homo sapien
4	2926	81.3	695	11 Q9J0J9	Q9J0J9 rattus norv
5	2905	80.8	697	11 Q9DBP0	Q9DBP0 mus musculu
6	2899	80.6	697	11 Q9Z290	Q9Z290 mus musculu
7	2851	79.3	693	6 Q27360	Q27360 bos taurus
8	2098	58.3	397	4 Q8N2K2	Q8N2K2 homo sapien
9	2093	58.2	674	13 Q9PT82	Q9PT82 xenopus lae
10	2083	57.9	674	13 Q9PT83	Q9PT83 xenopus lae
11	2080	57.8	643	13 Q9D8R7	Q9D8R7 cyprinus ca
12	2058	57.2	636	13 Q91237	Q91237 pseudopleur
13	2047	56.9	632	13 Q9PDS6	Q9PDS6 brachydanio
14	1959.5	54.5	631	13 Q9PTQ8	Q9PTQ8 brachydanio
15	1717	47.7	637	11 Q9D2V6	Q9D2V6 mus musculu
16	1706.5	47.4	653	6 Q28361	Q28361 didelphis m

17 1696 47.2 632 4 Q8N8W2
18 1529 42.5 599 4 Q8N130
19 1475.5 41.0 601 11 Q8K4R8
20 1112 30.9 252 11 Q8VI55
21 1046 29.1 290 13 Q9D8S2
22 1002 27.9 290 13 Q9D8S1
23 989 27.5 290 13 Q9D8S4
24 966.5 26.9 321 11 Q8C012
25 962 26.7 290 13 Q9D8S0
26 865 24.0 230 13 Q9D8R9
27 834 23.2 268 11 Q9QWL8
28 830 23.1 573 5 Q23530
29 814 22.6 230 13 Q9D8S5
30 773.5 21.5 337 11 Q9Z323
31 766 21.3 230 13 Q9D8S3
32 724 20.1 240 13 Q9D8R8
33 710.5 19.8 232 6 Q77701
34 559.5 15.6 382 16 Q87918
35 548.5 15.2 386 16 Q8DES1
36 418.5 11.6 388 16 Q8NM36
37 393.5 10.9 474 16 Q8FMC5
38 285.5 7.9 327 11 Q9Z322
39 283 7.9 555 16 Q99XA9
40 280.5 7.8 543 16 Q99YH9
41 277.5 7.7 543 16 Q8NZW2
42 276.5 7.7 602 16 Q8D4M4
43 274.5 7.6 544 16 Q8Y8R8
44 263.5 7.3 543 16 Q97892
45 262.5 7.3 543 16 Q8DQX9

ALIGNMENTS

RESULT 1

Q9P0V7 ID Q9P0V7 PRELIMINARY; PRT; 689 AA.
AC Q9P0V7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sodium dependent phosphate transporter isoform Nap1-11b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=20079161; PubMed=10610722;
RA Xu H., Bai L., Collins J.F., Ghishan F.K.;
RT "Molecular cloning, functional characterization, tissue distribution,
RT and chromosomal localization of a human, small intestinal sodium-
RT phosphate (Na+-Pi) transporter (SLC34A2).";
RL Genomics 62:281-284(1999).
DR EMBL; AF146796; AAF31328.1; -
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR003841; Na/Pi_cotranspt.
DR Pfam; PF02690; Na_Pi_cotrans; 2.
DR TIGRFAms; TIGR01013; 2a58; 1.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
SQ SEQUENCE 689 AA; 75613 MW; 791CE76D36BD3F5 CRC64;

Query Match 99.9%; Score 3594; DB 4; Length 689;
Best Local Similarity 99.9%; Pred. No. 1.6e-252;
Matches 688; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPPELGDAQPNPKYLEGAGQOPTADPKSKTNKNTAPVTKIELPVSATLID 60
Db 1 MAPPELGDAQPNPKYLEGAGQOPTADPKSKTNKNTAPVTKIELPVSATLID 60
Qy 61 EPTVEDDNNWLTLDQSDGKWSRDTKGILCFQFGIGRLILIGFLYFVCSLDLTSSA 120

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Db 61 EPTVEDDPNNLFTLQDSGIKWSERDTKGKILCFQGIKRLILLGLFYFFVCSLDLSSA 120
Qy 121 FQLVGGKAGQFFNSNNSIMNPLGLGVIGLVTVLVQSSSTSTSIYVSWSSSLITVRAA 180
Db 121 FQLVGGKAGQFFNSNNSIMNPLGLGVIGLVTVLVQSSSTSTSIYVSWSSSLITVRAA 180
Qy 181 IPIIMGANIGTSINTI VALMOYVGRSEPRFAGATVHDFPNWLSYLVLLPVEVATHYL 240
Db 181 IPIIMGANIGTSINTI VALMOYVGRSEPRFAGATVHDFPNWLSYLVLLPVEVATHYL 240
Qy 241 EIIITQILVSEHFHFKNGEDAPLLKVIITKPTKLIIVOLDKKVISQIANDKAKNKSILVKI 300
Db 241 EIIITQILVSEHFHFKNGEDAPLLKVIITKPTKLIIVOLDKKVISQIANDKAKNKSILVKI 300
Qy 301 WCKTFTNKQINVTVPSTANCTSPSLCWTGDIQNTWTKNVTYKENTAKCOHIFVNFHLPD 360
Db 301 WCKTFTNKQINVTVPSTANCTSPSLCWTGDIQNTWTKNVTYKENTAKCOHIFVNFHLPD 360
Qy 361 LAVGTILLILSLVLCGCLIMVKILGSLVKGQVATVIKKTINTDPPFPFAMLTGYLAIL 420
Db 361 LAVGTILLILSLVLCGCLIMVKILGSLVKGQVATVIKKTINTDPPFPFAMLTGYLAIL 420
Qy 421 VAGAGTTFVQSSSVFTSALTPLIGVITIERAYPLTIGSNIGTTHAILAALASPGNAL 480
Db 421 VAGAGTTFVQSSSVFTSALTPLIGVITIERAYPLTIGSNIGTTHAILAALASPGNAL 480
Qy 481 RSLQIALCHFFNFISGILLWYPIPTPLPIRMAGLGNISAKYRWFVAVFYLIIFFFLI 540
Db 481 RSLQIALCHFFNFISGILLWYPIPTPLPIRMAGLGNISAKYRWFVAVFYLIIFFFLI 540
Qy 541 LTVFGLSLAGRVLVGVVGPVVFIIILVLCRLQSRCPVLPKQLQNNFPLNWRSLK 600
Db 541 LTVFGLSLAGRVLVGVVGPVVFIIILVLCRLQSRCPVLPKQLQNNFPLNWRSLK 600
Qy 601 PWDVAVSKFTGCFQMRCCCRVCCACCLLGGCKCCCKCEDLEEAQGGQDVPVK 660
Db 601 PWDVAVSKFTGCFQMRCCCRVCCACCLLGGCKCCCKCEDLEEAQGGQDVPVK 660
Qy 661 PETFDNITISREAQGEVPASDSKTECTAL 689
Db 661 PETFDNITISREAQGEVPASDSKTECTAL 689

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RESULT 2

```

ID O95436 PRELIMINARY; PRT; 690 AA.
AC O95436;
DT 01-MAY-1999 (TREMELrel. 10, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Sodium dependent phosphate transporter isoform NAPI-3B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine, and Lung;
RA Feild J.A., Dellapenna K.A., Edwards R.M.;
RT "Cloning and characterization of a sodium dependent phosphate
RT transporter isoform expressed in human small intestine and lung."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases..
DR EMBL; AF111856; AAC98695.1; -.
DR EMBL; AF111856; AAC98695.1; -.
DR Genbank; HGNC:11020; SLC34A2.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR003841; Na/F1_cotransp.
DR Pfam; PF02690; Na_F1_cotrans; 2.
DR TIGRFAMs; TIGR01013; 2a58; 1.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
SQ SEQUENCE 690 AA; 75761 MW; BAC4F7D1C992D5C0 CRC64;

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Query Match 99.3%; Score 3570.5; DB 4; Length 690;
 Best Local Similarity 99.6%; Pred. No. 7.9e-251;

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Matches 687; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
Qy 1 MAPPELGDQPNPDKVLGSAAGQOPTAPDKSKETNK-NNTTEAPTKIELLPSYSTATLI 59
Db 1 MAPPELGDQPNPDKVLGSAAGQOPTAPDKSKETNK-NNTTEAPTKIELLPSYSTATLI 60
Qy 60 DEPTVEDDPNNLFTLQDSGIKWSERDTKGKILCFQGIKRLILLGLFYFFVCSLDLSS 119
Db 61 DEPTVEDDPNNLFTLQDSGIKWSERDTKGKILCFQGIKRLILLGLFYFFVCSLDLSS 120
Qy 120 AFQLVGGKAGQFFNSNNSIMNPLGLGVIGLVTVLVQSSSTSTSIYVSWSSSLITVRA 179
Db 121 AFQLVGGKAGQFFNSNNSIMNPLGLGVIGLVTVLVQSSSTSTSIYVSWSSSLITVRA 180
Qy 180 APTIIMGANIGTSINTI VALMOYVGRSEPRFAGATVHDFPNWLSYLVLLPVEVATHY 239
Db 181 APTIIMGANIGTSINTI VALMOYVGRSEPRFAGATVHDFPNWLSYLVLLPVEVATHY 240
Qy 240 LEIITQILVSEHFHFKNGEDAPLLKVIITKPTKLIIVOLDKKVISQIANDKAKNKSILVK 299
Db 241 LEIITQILVSEHFHFKNGEDAPLLKVIITKPTKLIIVOLDKKVISQIANDKAKNKSILVK 300
Qy 300 IWCKTFTNKQINVTVPSTANCTSPSLCWTGDIQNTWTKNVTYKENTAKCOHIFVNFHLP 359
Db 301 IWCKTFTNKQINVTVPSTANCTSPSLCWTGDIQNTWTKNVTYKENTAKCOHIFVNFHLP 360
Qy 360 DIAVGTILLILSLVLCGCLIMVKILGSLVKGQVATVIKKTINTDPPFPFAMLTGYLAI 419
Db 361 DIAVGTILLILSLVLCGCLIMVKILGSLVKGQVATVIKKTINTDPPFPFAMLTGYLAI 420
Qy 420 LVGAGMTFVQSSSVFTSALTPLIGVITIERAYPLTIGSNIGTTHAILAALASPGNA 479
Db 421 LVGAGMTFVQSSSVFTSALTPLIGVITIERAYPLTIGSNIGTTHAILAALASPGNA 480
Qy 480 LBSSLOIALCHFFNFISGILLWYPIPTPLPIRMAGLGNISAKYRWFVAVFYLIIFFFLI 539
Db 481 LBSSLOIALCHFFNFISGILLWYPIPTPLPIRMAGLGNISAKYRWFVAVFYLIIFFFLI 540
Qy 540 PLTVFGLSLAGRVLVGVVGPVVFIIILVLCRLQSRCPVLPKQLQNNFPLNWRSL 599
Db 541 PLTVFGLSLAGRVLVGVVGPVVFIIILVLCRLQSRCPVLPKQLQNNFPLNWRSL 600
Qy 600 KPDVAVSKFTGCFQMRCCCRVCCACCLLGGCKCCCKCEDLEEAQGGQDVPVK 659
Db 601 KPDVAVSKFTGCFQMRCCCRVCCACCLLGGCKCCCKCEDLEEAQGGQDVPVK 660
Qy 660 APTFDNITISREAQGEVPASDSKTECTAL 689
Db 661 APTFDNITISREAQGEVPASDSKTECTAL 690

```

RESULT 3

```

ID Q8WYA9 PRELIMINARY; PRT; 591 AA.
AC Q8WYA9;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Sodium-phosphate transporter (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RA Xu H., Bai L., Collins J.F., Ghislan F.K.;
RT "Molecular cloning, functional characterization of a human intestinal
RT sodium-phosphate transporter gene promoter and its gene structure."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF234245; AAL55657.1; -.
DR EMBL; AF234237; AAL55657.1; JOINED.
DR EMBL; AF234238; AAL55657.1; JOINED.

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DR EMBL; AF234239; AAL55657.1; JOINED.
 DR EMBL; AF234241; AAL55657.1; JOINED.
 DR EMBL; AF234242; AAL55657.1; JOINED.
 DR EMBL; AF234243; AAL55657.1; JOINED.
 DR EMBL; AF234244; AAL55657.1; JOINED.
 DR InterPro; IPR003841; Na/Pi cotranspt.
 DR Pfam; PF02690; Na/Pi cotrans. 2.
 DR TIGRFAMs; TIGR01013; 2a58; 1.
 FT NON_TER 591 591
 SQ SEQUENCE 591 AA; 64789 MW; 32AEC5C2B5098A7 CRC64;
 Query Match 84.0%; Score 3023; DB 4; Length 591;
 Best Local Similarity 99.8%; Pred. No. 3.6e-211;
 Matches 590; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPWPELGDAQPNPDKYLEGAAGQOPTAPDKSKETNNTEAPVTKIELLPSYSTATLID 60
 DB 1 MAPWPELGDAQPNPDKYLEGAAGQOPTAPDKSKETNNTEAPVTKIELLPSYSTATLID 60
 QY 61 EPTVEDDPWNLPTLDQSGIKWSEDTKGKILCFQGIKGLILLGLFLYFFVCSLDILSSA 120
 DB 61 EPTVEDDPWNLPTLDQSGIKWSEDTKGKILCFQGIKGLILLGLFLYFFVCSLDILSSA 120
 QY 121 POLVGGKMAQGFSSNSIMSNPLGLVIGLVTVLVQSSSTSTSIWSSSSLLTVRAA 180
 DB 121 POLVGGKMAQGFSSNSIMSNPLGLVIGLVTVLVQSSSTSTSIWSSSSLLTVRAA 180
 QY 181 IPIITMGANIGTSTNTVIALMQVGRSEFRFAGATVHDFNNWLSVLVLPVEVATHYL 240
 DB 181 IPIITMGANIGTSTNTVIALMQVGRSEFRFAGATVHDFNNWLSVLVLPVEVATHYL 240
 QY 241 EIIITOLIVSEFHFKNGEDAPDLKVIKTPFKLIVOLDKKVISOIAMDDEKAKKSLVKI 300
 DB 241 EIIITOLIVSEFHFKNGEDAPDLKVIKTPFKLIVOLDKKVISOIAMDDEKAKKSLVKI 300
 QY 301 WCKTFTNKTQINTVTVSTANTCPSLCSWTGDIQNWTKMKNVTKENIAKQHI FVNFHLP 360
 DB 301 WCKTFTNKTQINTVTVSTANTCPSLCSWTGDIQNWTKMKNVTKENIAKQHI FVNFHLP 360
 QY 361 LAVGTILLILSLVLCGLIMIVKILGSLVKGQVATVIKKTINTDPPFPFALWLTGYLAI 420
 DB 361 LAVGTILLILSLVLCGLIMIVKILGSLVKGQVATVIKKTINTDPPFPFALWLTGYLAI 420
 QY 421 VGAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTIGSNIGTITTTAILAALASFGNAL 480
 DB 421 VGAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTIGSNIGTITTTAILAALASFGNAL 480
 QY 481 RSSLQIALCHFFNFISSGILLWYPIPTPLPRMAKGLGNISAKYRWFAVYLIIFPFLIP 540
 DB 481 RSSLQIALCHFFNFISSGILLWYPIPTPLPRMAKGLGNISAKYRWFAVYLIIFPFLIP 540
 QY 541 LTVFGLSLAGWRVLVGVGVVVFIIILVLCRLQLQSRCPVLPKLQNNWF 591
 DB 541 LTVFGLSLAGWRVLVGVGVVVFIIILVLCRLQLQSRCPVLPKLQNNWF 591
 RESULT 4
 Q9J09 PRELIMINARY; PRT; 695 AA.
 AC Q9J09;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Type IIB sodium-phosphate transporter.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Lung;
 RX MEDLINE=20340494; PubMed=10880371;
 RA Hashimoto M., Wang D.-Y., Kamo T., Zhu Y., Tsujiuchi T., Konishi Y.,

RA Tanaka M., Sugimura H.;
 RT "Isolation and Localization of Type IIB Na/Pi Cotransporter in the
 RT Developing Rat Lung.";
 RL Am. J. Pathol. 157:21-27 (2000).
 DR EMBL; AF157026; AAF76291.1; -.
 DR InterPro; IPR003841; Na/Pi cotranspt.
 DR Pfam; PF02690; Na/Pi cotrans. 2.
 DR TIGRFAMs; TIGR01013; 2a58; 1.
 SQ SEQUENCE 695 AA; 75992 MW; 3FAFE827527E0061 CRC64;
 Query Match 81.3%; Score 2926; DB 11; Length 695;
 Best Local Similarity 80.5%; Pred. No. 4.9e-204;
 Matches 545; Conservative 66; Mismatches 64; Indels 2; Gaps 2;
 QY 1 MAPWPELGDAQPNPDKYLEGAAGQOPTAPDKSKETNNTEAPVTKIELLPSYSTATLII 59
 DB 1 MAPWPELGDAQPNPDKYLEGAAGQOPTAPDKSKETNNTEAPVTKIELLPSYSTATLII 60
 QY 60 DEPTVEDDPWNLPTLDQSGIKWSEDTKGKILCFQGIKGLILLGLFLYFFVCSLDILSS 119
 DB 61 EPTVEDDPWNLPTLDQSGIKWSEDTKGKILCFQGIKGLILLGLFLYFFVCSLDILSS 120
 QY 120 AFOLVGGKMAQGFSSNSIMSNPLGLVIGLVTVLVQSSSTSTSIWSSSSLLTVRAA 179
 DB 121 AFOLVGGKMAQGFSSNSIMSNPLGLVIGLVTVLVQSSSTSTSIWSSSSLLTVRAA 180
 QY 180 APTMGANIGTSTNTVIALMQVGRSEFRFAGATVHDFNNWLSVLVLPVEVATHYL 239
 DB 181 APTMGANIGTSTNTVIALMQVGRSEFRFAGATVHDFNNWLSVLVLPVEVATHYL 240
 QY 240 LEIITOLIVSEFHFKNGEDAPDLKVIKTPFKLIVOLDKKVISOIAMDDEKAKKSLVKI 299
 DB 241 LEKLTWLVLETFSEFNGEDAPDLKVIKTPFKLIVOLDKKVISOIAMDDEKAKKSLIK 300
 QY 300 IWCKTFTNKTQINTVTVSTANTCPSLCSWTGDIQNWTKMKNVTKENIAKQHI FVNFHLP 359
 DB 301 IWCKTFTNKTQINTVTVSTANTCPSLCSWTGDIQNWTKMKNVTKENIAKQHI FVNFHLP 360
 QY 360 DLAVGTILLILSLVLCGLIMIVKILGSLVKGQVATVIKKTINTDPPFPFALWLTGYLAI 419
 DB 361 DLAVGTILLILSLVLCGLIMIVKILGSLVKGQVATVIKKTINTDPPFPFALWLTGYLAI 420
 QY 420 LVGAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTIGSNIGTITTTAILAALASFGNA 479
 DB 421 LVGAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTIGSNIGTITTTAILAALASFGNT 480
 QY 480 LRSLQIALCHFFNFISSGILLWYPIPTPLPRMAKGLGNISAKYRWFAVYLIIFPFLI 539
 DB 481 LRSLQIALCHFFNFISSGILLWYPIPTPLPRMAKGLGNISAKYRWFAVYLIIFPFLI 540
 QY 540 PLTVFGLSLAGWRVLVGVGVVVFIIILVLCRLQLQSRCPVLPKLQNNWFPLWNRSL 599
 DB 541 PLTVFGLSLAGWRVLVGVGVVVFIIILVLCRLQLQSRCPVLPKLQNNWFPLWNRSL 600
 QY 600 KPMDAVVSKFTGCFQMRCCCRVCRACCLICGPKCCRCCKCEDLEAQQGVQVVK 659
 DB 601 KPMDNIISLATSFCORRCCCRVCRVCCWCGC-KCCRCGCKCKNLEEEKEQGVQVVK 659
 QY 660 APETRONIISREAOGE 676
 DB 660 ASGGFDNTAMSKECODE 676
 RESULT 5
 Q9DBP0 PRELIMINARY; PRT; 697 AA.
 ID Q9DBP0
 AC Q9DBP0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Solute carrier family 34 (Sodium phosphate), member 2.
 GN SLG34A2.
 OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito J., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schram L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boirelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoro N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK004632; BAB23600.1; -.
DR MGD; MGI:1342284; Slc34a2.
DR InterPro; IPR003841; Na/Pi cotranspt.
DR PFam; PF02690; Na_Pi_cotrans; 2.
DR TIGRFAMs; TIGR01013; 2a58; 1.
SQ SEQUENCE 697 AA; 76244 MW; 2A7B93384857BF16F CRC64;

Query Match 80.8%; Score 2905; DB 11; Length 697;
Best Local Similarity 80.0%; Pred. No. 1.6e-202;
Matches 543; Conservative 62; Mismatches 70; Indels 4; Gaps 3;

Qy 1 MAPPELGDAQPNPKYLEGAGQOPTAPDKSKETNK-NNTEAPVTKIELLPSTATLI 59
Db 1 MAPPELENAQPNPKYLEGAGQOPTAPDKSKETNK-NNTEAPVTKIELLPSTATLI 60
Qy 60 DEPTVEDDPAKLPLODQSGIKMSERDTKGKILCFQGIKRLILLGLYFFVCSLDLSS 119
Db 61 EEHPGTDEWDLPELODTGKIKMSERDTKGKILCFQGVKFIILLGLYFLVCSLDVSS 120
Qy 120 AFQLVGKMAQGFSSNSIMSNPLGLVIGLVTVLVQSSSTSTSIIVSMVSSLLTVRA 179
Db 121 AFQLVGKMAQGFSSNSIMSNPNVAGLVIGLVTVLVQSSSTSSIIIVSMVASSLLTVRA 180
Qy 180 APTIMGANGTSTNTIVALMQVGRSEFRAPAGATVHDFNNLSVLVLLPVEVATHY 239
Db 181 APTIMGANGTSTNTIVALMQAGDRNEFRAPAGATVHDFNNLSVFLVPLEATHY 240
Qy 240 LEITQLIVSEHFKNGEDAPDLKLVITKQPTKLIIVOLDKKVISOIAMNDEKAKNSLVK 299
Db 241 LEITANLVLETFKNGEDAPDLKLVITDPFTKLIILQDKKVIQIANGDSAAQKSLIK 300
Qy 300 INCKTFNKTQINVTVPSTNCTSPSYCWTGDIQNTWKNTYKNIACQHIFFNHP 359
Db 301 INCKSIINVTENVVTPSTNCTSPSYCWTGDIQNTWKNTYKNIACQHIFFNHP 360
Qy 360 DIAVGTILLISLVLCGLIMIVKLGSLKGVATVTKTINTDPPFPFAWLTGYLAI 419
Db 361 DIAVGIILLTVSLVLCGLIMIVKLGSLVGVATVTKTINTDPPFPFAWLTGYLAI 420
Qy 420 LVGAGMTIVQSSVFTSALTPILIGVITIERAYPLTGLSGNITGTTTTLAALASPGA 479
Db 421 LVGAGMTIVQSSVFTSMTPLIGVITIERAYPLTGLSGNITGTTTTLAALASPGA 480
Qy 480 LRSSIQIALCHFFPNIIGLIIWYPIPTFLPRMAKGLNISAKYRFAVFLIIFPFLI 539
Db 481 LRSSIQIALCHFFPNIIGLIIWYPIPTFLPRMAKGLNISAKYRFAVFLIIFPFPV 540

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Qy 540 PLATVFGLSAGWVVLGVGVVVFVFIILVLCLELLOSCRPVLPKLQNNFLPLMWSL 599
Db 541 PLATVFGLSAGWVVLGVGVVVFVFIILVLCLELLOSCRPVLPLKLFQNNFLPLMWSL 600
Qy 600 KPMDDAVSVKFTGCFQWRCRCCCRVCCACLLGCGPKCCRSKCCEDL--EEAQBGQDVP 657
Db 601 KPMDDVLSLATTFCQRRCCCRVCCVCCWVGCG-KCCRCSCKCRQGGEBEKEQDIP 659
Qy 658 VKAPEFDNITISREAOGE 676
Db 660 VKASGAFDNARMSKECODE 678
RESULT 6
Q92290 PRELIMINARY; PRT; 697 AA.
AC Q92290;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
DE Type IIb Na/phosphate-cotransporter.
GN SLc34A2 OR NPT2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Small intestine;
RX MEDLINE=99045724; PubMed=9826740;
RA Hilfinger H., Hattenhauser O., Traebert M., Forster I., Murer H.,
RA Biber J.;
RT "Characterization of a murine type II sodium-phosphate cotransporter
expressed in mammalian small intestine.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:14564-14569 (1998).
DR EMBL; AF081499; AAC80007.1; -.
DR MGD; MGI:1342284; Slc34a2.
DR InterPro; IPR003841; Na/Pi cotranspt.
DR PFam; PF02690; Na_Pi_cotrans; 2.
DR TIGRFAMs; TIGR01013; 2a58; 1.
SQ SEQUENCE 697 AA; 76286 MW; 8395ECCB0F565265 CRC64;

Query Match 80.6%; Score 2899; DB 11; Length 697;
Best Local Similarity 79.7%; Pred. No. 4.5e-202;
Matches 541; Conservative 64; Mismatches 70; Indels 4; Gaps 3;

Qy 1 MAPPELGDAQPNPKYLEGAGQOPTAPDKSKETNK-NNTEAPVTKIELLPSTATLI 59
Db 1 MAPPELENAQPNPKYLEGAGQOPTAPDKSKETNK-NNTEAPVTKIELLPSTATLI 60
Qy 60 DEPTVEDDPAKLPLODQSGIKMSERDTKGKILCFQGIKRLILLGLYFFVCSLDLSS 119
Db 61 EEHPGTDEWDLPELODTGKIKMSERDTKGKILCFQGVKFIILLGLYFLVCSLDVSS 120
Qy 120 AFQLVGKMAQGFSSNSIMSNPLGLVIGLVTVLVQSSSTSTSIIVSMVSSLLTVRA 179
Db 121 AFQLVGKMAQGFSSNSIMSNPNVAGLVIGLVTVLVQSSSTSSIIIVSMVASSLLTVRA 180
Qy 180 APTIMGANGTSTNTIVALMQVGRSEFRAPAGATVHDFNNLSVLVLLPVEVATHY 239
Db 181 APTIMGANGTSTNTIVALMQAGDRNEFRAPAGATVHDFNNLSVFLVPLEATHY 240
Qy 240 LEITQLIVSEHFKNGEDAPDLKLVITKQPTKLIIVOLDKKVISOIAMNDEKAKNSLVK 299
Db 241 LEITANLVLETFKNGEDAPDLKLVITDPFTKLIILQDKKVIQIANGDSAAQKSLIK 300
Qy 300 INCKTFNKTQINVTVPSTNCTSPSYCWTGDIQNTWKNTYKNIACQHIFFNHP 359
Db 301 INCKSIINVTENVVTPSTNCTSPSYCWTGDIQNTWKNTYKNIACQHIFFNHP 360
Qy 360 DIAVGTILLISLVLCGLIMIVKLGSLKGVATVTKTINTDPPFPFAWLTGYLAI 419

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Db 361 DLAVGILLTVSLVLCGLIMIVKLGSLVRCQVATVTKTANDPFFPFWMLTGYLAI 420
QY 420 LVGAGMTFVQSSSVFTSALTFLIGIVITIERAYPLTIGSNIGTITTAIALAASPNA 479
Db 421 LVGAGMTFVQSSSVFTSALTFLIGIVISIERAYPLTIGSNIGTITTAIALAASPNT 480
QY 480 LRSLQIALCHFFNFISGILLWYIPTRPIRMAGKLGNISAKRYWFAVYLIIFFFLI 539
Db 481 LRSLQIALCHFFNFISGILLWYIPTRPIRLAKGLGNISAKRYWFAVYLIIFFFVT 540
QY 540 PLTVFGLSLAGREVLVGVVPIIILVLCILRLQSRCPVLPKLQWNFILPIMWRSI 599
Db 541 PLTVFGLSLAGREVLVGVVPIIILVLCILRLQSRCPVLPLKLEDFLWNLPLWHSI 600
QY 600 KPMDAVVSFTGCFQMRCCCRVCCCRACCLCGCPKCRCKCEDL--EEAQBGQDVP 657
Db 601 KPMDNISLATTFCORRCCCRVCCCRVCCWVGC--KCRCKCRCKQGBEKEQDIP 659
QY 658 VKAPETFDNITISREAQGE 676
Db 660 VKASGAFDAAAMSKCODE 678

RESULT 7
Q27960
ID Q27960 PRELIMINARY; PRT; 693 AA.
AC Q27960;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sodium-dependent phosphate transporter.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95255303; PubMed=7737195;
RA Helps C.R., Murer H., McGiven J.D.;
RT "Cloning, sequence analysis and expression of the cDNA encoding a
RT sodium-dependent phosphate transporter from the bovine renal
RT epithelial cell line NBL-1."
RL Eur. J. Biochem. 228:927-930(1995).
DR EMBL; X81699; CAA57345.1; -.
DR InterPro; IPR003841; Na/Pi_cotransp.
DR Pfam; PF02690; Na_Pi_cotrans; 2.
DR TIGRFAMs; TIGR01013; 2a58; 1.
SQ SEQUENCE 693 AA; 75826 MW; 6B1CC17FE5C13213 CRC64;

Query Match 79.3%; Score 2851; DB 6; Length 693;
Best Local Similarity 76.3%; Pred. No. 1.3e-198;
Matches 53; Conservative 82; Mismatches 73; Indels 10; Gaps 3;

QY 1 MAPWPELGAQNPDKYLEGAAGQPTADPKSKETNNKNTAPVTKIELPFSYSTATLID 60
Db 1 MAPWPELENSQPTSEKYTVKADGQSAKPEKATEKDDTGTPTIKIELVPSSTATLIE 60
QY 61 EPTVEDDPNVLPTQDSGKWSERDYGKILCFQGIKILLGLLGLYFFVCSLDLSSA 120
Db 61 EPTVEDDPNVLPTQDSGKWSERDYGKILCFQGIKILLGLLGLYFFVCSLDLSSA 120
QY 121 FQLVGGHMAQGFSSNSTMPLGLVIGLVVLVQSSSTSTSVSWSSSLLTVRAA 180
Db 121 FQLVGGHMAQGFSSNSTMPLGLVIGLVVLVQSSSTSTSVSWSSSLLTVRAA 180
QY 181 IPIIMGANIGTSTITVALMQGDRSEFRFAFAGTVHDFNWLVLVLLPVEVATHYL 240
Db 181 IPIIMGANIGTSTITVALMQGDRSEFRFAFAGTVHDFNWLVLVLLPVEVATHYL 240
QY 241 EITQITVSEFFHKGEDAPOLLKVIITKPTFKLIVOLDKKVISQIAMNDEKAKNSLVKI 300
Db 241 EITQITVSEFFHKGEDAPOLLKVIITKPTFKLIVOLDKKVISQIAMNDEKAKNSLVKI 300

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Db 241 ERTNLVSEFFHKGGEAPELLKVIITKPTFKLIVOLDKKVISQIAMNDEKAKNSLVKI 300
QY 301 WKCTFTNKQIINVTVPSSTANTCSPSLCWTGDIQNTWTKNVTYKENIAKCOHIFWNFLPD 360
Db 301 WKCTFTNKQIINVTVPSSTANTCSPSLCWTGDIQNTWTKNVTYKENIAKCOHIFWNFLPD 360
QY 361 LAVGTILLLSLLVLCGLIMIVKLGSLVRCQVATVTKTANDPFFPFWMLTGYLAI 420
Db 361 LAVGTILLLSLLVLCGLIMIVKLGSLVRCQVATVTKTANDPFFPFWMLTGYLAI 420
QY 421 VGAGMTFVQSSSVFTSALTFLIGIVITIERAYPLTIGSNIGTITTAIALAASPNA 480
Db 421 VGAGMTFVQSSSVFTSALTFLIGIVISIERAYPLTIGSNIGTITTAIALAASPNT 480
QY 481 RSSLQIALCHFFNFISGILLWYIPTRPIRMAGKLGNISAKRYWFAVYLIIFFFLI 540
Db 481 RSSLQIALCHFFNFISGILLWYIPTRPIRLAKGLGNISAKRYWFAVYLIIFFFVT 540
QY 541 LTVPFGLSLAGREVLVGVVPIIILVLCILRLQSRCPVLPKLQWNFILPIMWRSI 600
Db 541 LAVFGLSLIGWPLVNGVASPIVLVLLVVLVVKILQSPFCGSLPKQLRSDFLPFWMSLE 600
QY 601 PWDAAVSKFTGCFQMRCCCRVCCCRACCLCGCPKCRCKCEDL--EEAQBGQDVPVKA 660
Db 601 PWDKLTSLTSCFQMRCCCRVCCCRVCCWVGC--KCRCKCRCKQGBEKEQDIP 657
QY 661 PETFDNITISREAQ--GSPASDSK--TECTAL 689
Db 658 PEAFNNLMDKRAQGVTKSEVDASGTVKIVSSVTAL 693

RESULT 8
Q8N2K2
ID Q8N2K2 PRELIMINARY; PRT; 397 AA.
AC Q8N2K2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90534.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Ovarian carcinoma;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075015; BAC11354.1; -.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR TIGRFAMs; TIGR01013; 2a58; 1.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 397 AA; 43726 MW; 23D42CBFC9555458 CRC64;

Query Match 58.3%; Score 2098; DB 4; Length 397;
Best Local Similarity 98.3%; Pred. No. 3.2e-144;
Matches 396; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 287 MNDEKAKNSLVKWKCTFTNKQIINVTVPSSTANTCSPSLCWTGDIQNTWTKNVTYKENI 346
Db 1 MNDEKAKNSLVKWKCTFTNKQIINVTVPSSTANTCSPSLCWTGDIQNTWTKNVTYKENI 346
QY 347 AKCOHIFWNFLPDIAVGTILLLSLLVLCGLIMIVKLGSLVRCQVATVTKTANDP 406
Db 61 AKCOHIFWNFLPDIAVGTILLLSLLVLCGLIMIVKLGSLVRCQVATVTKTANDP 406

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QY 407 PFFAWLTYLAILVAGMTFIVOSSVFTSALTPLIGIVITIERAYPLTLGSGTGT 466
DB 121 PFFAWLTYLAILVAGMTFIVOSSVFTSALTPLIGIVITIERAYPLTLGSGTGT 180
QY 467 TAILAALASFGNALRSSLOIALCHFFFNISGILLWTPPTPLPIRMAKGLGNISAKYRW 526
DB 181 TAILAALASFGNALRSSLOIALCHFFFNISGILLWTPPTPLPIRMAKGLGNISAKYRW 240
QY 527 FAVFYLLIFFELIPLTVFGLSLAGRWLVGVVVFIIILVLCILLOQRCPRLPKL 586
DB 241 FAVFYLLIFFELIPLTVFGLSLAGRWLVGVVVFIIILVLCILLOQRCPRLPKL 300
QY 587 QNNWFLPLNWSLKPWDAVSKFTGCFQMRCCCCCRVCCACCLLGCPCCKCCKCED 646
DB 301 QN-----NWSLKPWDAVSKFTGCFQMRCCCCCRVCCACCLLGCPCCKCCKCED 354
QY 647 LEEAQEGQDVPVKAPETFDNITISREAQGEVPASDSKTECTAL 689
DB 355 LEEAQEGQDVPVKAPETFDNITISREAQGEVPASDSKTECTAL 397

RESULT 9
Q9PT82
ID Q9PT82 PRELIMINARY; PRT; 674 AA.
AC Q9PT82;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Sodium phosphate cotransporter.
GN XNAPI-B.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=97248089; PubMed=9094212;
RA Ishizuwa-Oka A., Stolor M.A., Ueda S., Shi Y.B.;
RT "Temporal and spatial expression of an intestinal Na+/PO4 3-
cotransporter correlates with epithelial transformation during thyroid
RT hormone-dependent frog metamorphosis.";
RL Dev. Genet. 20:53-66(1997).
DR EMBL; L78836; AAF21135.1;
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000005; HTHAc.
DR Pfam; PF02690; Na_Pi_cotransp.
DR TIGRFAMs; TIGR01013; 2a58; 1.
DR PROSITE; PS00022; EGF 1; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY 1; 1.
SQ SEQUENCE 674 AA; 73837 MW; 70CE7520C98E73F1 CRC64;

Query Match 58.2%; Score 2093; DB 13; Length 674;
Best Local Similarity 61.5%; Pred. No. 1.4e-143;
Matches 428; Conservative 90; Mismatches 134; Indels 44; Gaps 13;

QY 1 MAPWPELGDAQPNPKYLEG-----AAGQQTAPDKSKETKNKNTTEAPVTKIELLPYST 55
DB 1 MPPFPEIDNHFNTGVDYDSDSKFVWSTGTVNPNVND-----GTPSDPEK-ELSPYST 51
QY 56 ATL-----IDPEVDDPNLPTLQDSIKWSDRTKGLCFQFQIGRLILLAGLYEFVC 112
DB 52 LSLCKETPEPEV-DPMDPELKSSTGPKWAEWTKQRLSVLGLWVKSLLVTLILYFVC 110
QY 113 SLDILSSAFQLVGGKAGOFFNSNIMNPLIGVILVTVLVQSSSTSTSIIVSWSS 172
DB 111 SLDILSSAFQLVGGKAGDIFKNHSLVSNPVAGIVIGVTLVTVLVQSSSTSTSIIVSWSS 170
QY 173 SLLTVRAAIPITMANGTSTNTIVVALMQVDSERFRAPAGATVHDFNWLVLVLLP 232
DB 171 NILTVRSAPITMANGTSTNTIVVALMQSDRNEFRAPAGATVHDFNWLVLVLLP 230

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QY 233 VEVATHLEIITOLIVSRHFKNGEDAPDLKLVITKPTKLIIVOLDKKVISQIANDEKA 292
DB 231 IEVATGLFHLTSALVKSNIQTQDAPDMLKVIITEPLTKGIIQDQKVIQDIANGDPLA 290
QY 293 KNSLVKIVCKTFTNKTQINVTVPSTANTCTSPSLCWTGDIQNTWTKNTYKEMI-----AK 348
DB 291 QNKSLLIKKEC---SYKTIVNISLPSAENCTSLCWTDD-----NNVTGTFETIKYK 341
QY 349 CQHIFVNFHPLDPLAVGTILLILSLVLCGLIMIVKILGSLVKGOVATVIKKTINTDPPF 408
DB 342 CSHFSTWPLDPLAVGLILLALSFLVLCVLIHVKILNSLKGQSVLKKVINTDPPF 401
QY 409 PFAWLGYLAILVAGMTFIVQSSVFTSALTPLIGIVITIERAYPLTLGSGTGT 468
DB 402 PFWLGYLAMLVAGMTFIVQSSVFTSALTPLIGIVISIERAYPLTLGSGTGT 461
QY 469 ILAALASPGNALRSSLOIALCHFFFNISGILLWTPPTPLPIRMAKGLGNISAKYRWA 528
DB 462 LLAALASPGETLQNSVQIALCHFFFNISGIIIVYPIPFMRPIPIRLAKGLGNKTAKYRWA 521
QY 529 VFYLLIFFELIPLTVFGLSLAGRWLVGVVVFIIILVLCILLOQRCPRLPKLQW 588
DB 522 VVYLILCFILMPLVGLSVAGQALVGVAVPVTMIVAVISVNVLSQKWPRIPLPKD 581
QY 589 WNFPLWMSLKPWDA-VVSKFTGCFQMRCCCCCRVCCACCLLGCPCCKCCKCEDL 647
DB 582 WDFLPKWHSLKPWDA-CMLGASLWCKQF-CGCCCGKHCKGC-----KCC---KCHDK 630
QY 648 EEAQEGQDVPVKAPETFDNITISREAQGEVPASDSK 683
DB 631 EDEECDIETKPOALEHNDV-IDLSDEIKKPESDEQ 665

RESULT 10
Q9PT83
ID Q9PT83 PRELIMINARY; PRT; 674 AA.
AC Q9PT83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Sodium phosphate cotransporter.
GN XNAPI-A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=97248089; PubMed=9094212;
RA Ishizuwa-Oka A., Stolor M.A., Ueda S., Shi Y.B.;
RT "Temporal and spatial expression of an intestinal Na+/PO4 3-
cotransporter correlates with epithelial transformation during thyroid
RT hormone-dependent frog metamorphosis.";
RL Dev. Genet. 20:53-66(1997).
DR EMBL; L78835; AAF21134.1;
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000005; HTHAc.
DR InterPro; IPR003841; Na/Pi_cotransp.
DR Pfam; PF02690; Na_Pi_cotrans; 2.
DR TIGRFAMs; TIGR01013; 2a58; 1.
DR PROSITE; PS00022; EGF 1; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY 1; 1.
SQ SEQUENCE 674 AA; 73818 MW; E34B7809A346B5F4 CRC64;

Query Match 57.9%; Score 2083; DB 13; Length 674;
Best Local Similarity 61.1%; Pred. No. 7.3e-143;
Matches 425; Conservative 93; Mismatches 134; Indels 44; Gaps 13;

QY 1 MAPWPELGDAQPNPKYLEG-----AAGQQTAPDKSKETKNKNTTEAPVTKIELLPYST 55

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Db 1 MPPPEIDNHEGFTGVDYDDSKPVNWTGINVPND-----GTPSDPEK-ELSPYISA 51
Qy 56 ATL-----IDPEYVDDPNNLPTLQDSGIKWSERDTKGLCFQIGRLLILLGLYEFVC 112
Db 52 LSLCKETPEPEEV-DPNDMPKSTGPKWAEMTTKQRIISLVLLGWKSVLLVTLTYFFVC 110
Qy 113 SLDLILSSAFQVGGKMGAGOFFNSISMSNPILGLVIGVLTVLVQSSSTSTSVVSVSS 172
Db 111 SLDLILSSAFQVGGKAGDFIKHNSVLNPNVAGIVIGVLTVLVQSSSTSTSVVSVSS 170
Qy 173 SLLTVRAAIPITMANGNISINTVALMOQVDRSEFRAPAGATVHDFNWLVLVILP 232
Db 171 NLTIVRSAPITMANGNISINTVALMOQVDRSEFRAPAGATVHDFNWLVLVILP 230
Qy 233 VEVATHYLEITOLIVESHFHKNGEDAPDLKVKITKPTKLIIVOLDKKVISOIAMNDEKA 292
Db 231 IEVATGYLHLSITVSKFSNIQTQDAPDLKVKITEPLTKIIIDTQVIRDIATGDPAPAKNSLIKI 279
Qy 293 KNSLIVKIKWCTFNKTQINVTVPSTACTSPSLCWTGDIQNTWTKNVTYKENI---AK 348
Db 291 QNKSIIKKEC---SYKTLVNI SLPSAENCTASLCTWDD-----NNVTWTEGFETIKVX 341
Qy 349 QHIFPNPHLDIAVGNPILILSLVLGCLIMVILKGLSVLKGQVATVTKTINTDPPF 408
Db 342 CSHLPASTNLPDLAVGLIILALSFLVLCVCLILVILKILNSLLKGOVSLIKKVINTDPPF 401
Qy 409 PEAULTGYLALLVAGMTRFIVQSSSVFTSALTTELIGIGVITIERAYPLTGLSGNIGTTT 468
Db 402 PFSWITGYLMLVAGMTRFIVQSSSVFTSALTTELIGIGVITIERAYPLTGLSGNIGTTT 461
Qy 469 ILAALASPAGNALSRLQIALCHFFNFISGILIMVPIPTLRPIRMAGLGNISAKYRWF 528
Db 462 LLAALASGETLQNSVQIALCHFFNFISGILIMVPIPTLRPIRMAGLGNISAKYRWF 521
Qy 529 VYLIIFPFLPLVFGSLAGNRVLVGVGVVVFIIILVLCRLLOSCRPVLPKQLQN 588
Db 522 VYLIIFPFLPLVFGSLAGNRVLVGVGVVVFIIILVLCRLLOSCRPVLPKQLQN 581
Qy 589 WNFPLNMRSLKPDWA-VVSKFTGCFQMECCCVCCACCLLGCPCRCCKCEDL 647
Db 582 WDFLPKWHSLKPDWACMLGASLWCKQF-CCCCGKCKG-----KCC---KCHDK 630
Qy 648 EBAQSGQVDPKAPETFDNITISREAAQGEVPASDK 683
Db 631 EDECDIETKQALEHNDV-IDLSDEIKKPSDQ 665

RESULT 11
Q9DDR7 PRELIMINARY; PRT; 643 AA.
AC Q9DDR7;
DT 01-MAR-2001 (TRENDELrel. 16, Created)
DT 01-MAR-2001 (TRENDELrel. 16, Last sequence update)
DT 01-MAR-2003 (TRENDELrel. 23, Last annotation update)
DE Na/Pi cotransporter Napi-1b2 (Fragment)
OS Cyprinus carpio (Common carp)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
RN TISSUE=Kidney;
RP SEQUENCE FROM N.A.
RA "The evolution of the Na/Pi cotransport systems.";
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF2971189; AAG35803.1; -
DR InterPro; IPR003841; Na/Pi cotranspt.
DR Pfam; PF02690; Na Pi cotrans; 2.
DR TIGRfams; TIGR01013; 2a58; 1.
FT NON TER 1
SQ SEQUENCE 643 AA; 70626 MW; 7ABD66060F687031 CRC64;

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Query Match 57.8%; Score 2080; DB 13; Length 643;
Best Local Similarity 64.5%; Pred. No. 1.le-142;
Matches 401; Conservative 82; Mismatches 117; Indels 22; Gaps 2;

Qy 61 BPTVEDPNNLPTLQDSGIKWSERDTKGLCFQIGRLLILLGLYEFVCSDILSSA 120
Db 40 EPBEVDPNNLPTLQDSGIKWSERDTKGLCFQIGRLLILLGLYEFVCSDILSSA 99
Qy 121 POLVGGKMGAGOFFNSISMSNPILGLVIGVLTVLVQSSSTSTSVVSWSSLLTVRAA 180
Db 100 POLVGGKMGAGOFFNSISMSNPILGLVIGVLTVLVQSSSTSTSVVSWSSLLTVRAA 159
Qy 181 IPIIMANGNISINTVALMOQVDRSEFRAPAGATVHDFNWLVLVILPVEVATHYL 240
Db 160 VPIIMANGNISINTVALMOQVDRSEFRAPAGATVHDFNWLVLVILPVEVATHYL 219
Qy 241 ELIITOLIVESHFHKNGEDAPDLKVKITKPTKLIIVOLDKKVISOIAMNDEKAKNSLVIKI 300
Db 220 YRLTKLIIDSFNITQDAPDLKVKITEPLTKIIIDTQVIRDIATGDPAPAKNSLIKI 279
Qy 301 WCKTFTNKTQINVTVPSTACTSPSLCWTGDIQNTWTKNVTYKENIACQHIIFVNFHLPD 360
Db 280 WCKTFTNKTQINVTVPSTACTSPSLCWTGDIQNTWTKNVTYKENIACQHIIFVNFHLPD 339
Qy 361 LAVGTILLILSLVLCGCLIMVILKGLSVLKGQVATVTKTINTDPPFPFALVGYLAIL 420
Db 340 LAVGTILLILSLVLCGCLIMVILKGLSVLKGQVATVTKTINTDPPFPFALVGYLAIL 399
Qy 421 VQAGMTRFIVQSSSVFTSALTTELIGIGVITIERAYPLTGLSGNIGTTTILALASPAGN 480
Db 400 VQAGMTRFIVQSSSVFTSALTTELIGIGVITIERAYPLTGLSGNIGTTTILALASPAGN 459
Qy 481 RSSLIQIALCHFFNFISGILIMVPIPTLRPIRMAGLGNISAKYRWFVLYLIIFPFLIP 540
Db 460 ANSLOISLCHFFNFISGILIMVPIPTLRPIRMAGLGNISAKYRWFVLYLIIFPFLIP 519
Qy 541 IFTVFGSLAGNRVLVGVGVVVFIIILVLCRLLOSCRPVLPKQLQNWFPLMWSLK 600
Db 520 IFTVFGSLAGNRVLVGVGVVVFIIILVLCRLLOSCRPVLPKQLQNWFPLMWSLK 579
Qy 601 PDAVSVKFTGCFQMECCCVCCACCLLGCPCRCCKCEDLEAAGQGVV-- 658
Db 580 PDAVSVKFTGCFQMECCCVCCACCLLGCPCRCCKCEDLEAAGQGVV-- 619
Qy 659 KAPETFDNITISREAAQGEVPAS 680
Db 620 KAPETFDNITISREAAQGEVPAS 641

RESULT 12
Q91237 PRELIMINARY; PRT; 636 AA.
AC Q91237; O13231; O13174;
DT 01-NOV-1996 (TRENDELrel. 01, Created)
DT 01-NOV-1996 (TRENDELrel. 01, Last sequence update)
DT 01-MAR-2003 (TRENDELrel. 23, Last annotation update)
DE Na/Pi cotransport system protein.
OS Pseudopleuronectes americanus (Winter flounder) (Pleuronectes americanus)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Pleuronectidae; Pseudopleuronectes.
NCBI_TaxID=8265;
RN TISSUE=Intestine;
RP SEQUENCE FROM N.A.
RA "The evolution of the Na/Pi cotransport systems.";
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF2971189; AAG35803.1; -
DR InterPro; IPR003841; Na/Pi cotranspt.
DR Pfam; PF02690; Na Pi cotrans; 2.
DR TIGRfams; TIGR01013; 2a58; 1.
FT NON TER 1
SQ SEQUENCE 643 AA; 70626 MW; 7ABD66060F687031 CRC64;

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RESULT 15
O9D2V6

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Db 331 -----MEKNHIFVDTGPDPLAVGLLILLAGSLVWLCTCLILVYKMLNSLX 376
Qy 392 GQVATVIKKTINTDPPFPFPAWLTGYLAILVAGMTFIVQSSSVFTSALTPLIGIVITIE 451
Db 377 GQVAVIQKVINTDPPAPFTWVGYFAMVVGASMTFVQSSSVFTSALTPLIGLVISIE 436
Qy 452 RAYPLTLGSGNIGTTTTAILAALASPCNALRSSLOIALCHREFFNISGILLWYPIPTRLPI 511
Db 437 RAYPLTLGSGNIGTTTTAILAALASPREKLSSSFQALCHFFFNISGILLWYPIPTRLPI 496
Qy 512 RMAKGLGNISAKYRWFAVYLIIFFFELIPLTVFGLSLAGKXVLYGVGVFVFIILVLCL 571
Db 497 RMAKALGKETAKYRWFAVYLIIVCFLLPLSLVFGISMAGQAMVGVGCTPFGALLAFVIV 556
Qy 572 RLQSRCPVLPKLOQWNFPLWMSLXPDWAVSKFTGCF 613
Db 557 NVLQSRSPGHLPKWLQTWDFLPRWMSLQPLDGLITRATLCY 598
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Job time : 123 secs